

GenCore version 5.1.6									
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Run on:	June 7, 2005, 08:48:08	:	Search time	34.7668 Seconds					
Title:	Perfect score: US-10-000-439-2	(without alignments)							
Sequence:	1 ASTKGPSVFLPAPSSKSTSG.....MEALHNHYQQLSISPGK 330	913.271 Million cell updates/sec							
Scoring table:	BLOSUM62								
Searched:	Gapop 10.0 , Gapext 0.5								
Total number of hits satisfying chosen parameters:	283416								
Minimum DB seq length:	0								
Maximum DB seq length:	200000000								
Post-processing:	Minimum Match 0%								
Database :	Maximum Match 100%								
	Listing first 45 summaries								
PIR 79:*									
1: Piri:*									
2: pir2:*									
3: pir3:*									
4: pir4:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query	% Match	Length	DB ID	Description	ALIGNMENTS		
1	1729	98.0	330	1	GHHU	Ig gamma-1 chain C	RESULT 1		
2	1592.5	90.3	377	2	A23511	Ig gamma-3 chain C	GHHU		
3	1590.5	90.2	377	2	A60764	Ig gamma-3 chain C	Ig gamma-sapiens (man)		
4	1566	88.8	326	1	G2HU	Ig gamma-2 chain C	C;Species: Homo sapiens (man)		
5	1522.5	88.0	327	1	G4HU	Ig gamma-4 chain C	C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004		
6	1225.5	69.5	374	2	S69339	Ig heavy chain V <sub>r</sub>	C;Accession: A93433; S36611; S33887; B90563; A90564; B91668; A91723; A02146		
7	1225	69.4	328	1	I47159	Ig gamma 2a chain	R;Ellison, J.W.; Berson, B.J.; Hood, L.E.		
8	1222	69.3	255	4	S31866	Ig gamma-1 chain C	Nucleic Acids Res. 10, 4071-4079, 1982		
9	1219	69.1	328	2	I47160	Ig gamma-3 chain C	A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.		
10	1215	68.9	324	1	PT0207	Ig gamma-2 chain C	A;Reference number: A93433; MUID:8301943; PMID:681139		
11	1193	67.6	328	2	I47158	Ig gamma-4 chain C	A;Accession: S33887		
12	1192.5	67.6	323	1	GHRB	Ig heavy chain V <sub>r</sub>	A;Molecule type: DNA		
13	1189	67.4	328	1	I47161	Ig gamma 2a chain	A;Cross-references: EMBL:217370		
14	1174.5	66.6	329	1	G2GP	Ig gamma-1 chain C	R;Takashashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Honjo, T.		
15	1163.5	66.0	472	2	S31459	Ig gamma-2 chain C	Cell 29, 671-679, 1982		
16	1144.5	64.9	470	2	S31459	Ig gamma-1 chain C	A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a		
17	1125.5	63.8	308	2	C30554	Ig gamma-1 chain C	A;Reference number: S33887; MUID:8301943; PMID:681139		
18	1123	63.7	289	1	G3HWTI	Ig gamma-3 chain C	R;Cunningham, B.A.; Rutishauser, U.; Gall, W.B.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,		
19	1117.5	63.4	333	2	PS0018	Ig gamma-2b chain	Biochemistry 9, 3171-3181, 1970		
20	1116	63.3	444	2	PC4436	monoclonal antibody	A;Title: The covalent structure of a human gamma <sub>1</sub> -immunoglobulin. VII. Amino acid sequence		
21	1114	63.2	326	2	PS0017	Ig gamma-1 chain C	A;Reference number: A90564; MUID:71064025; PMID:5530842		
22	1109	62.9	324	1	G1MS	Ig gamma-1 chain C	A;Contents: Eu		
23	1108	62.8	329	1	G3MSC	Ig gamma-3 chain C	A;Accession: A90564		
24	1104	62.6	393	1	G1MSM	Ig gamma-1 chain C	A;Molecule type: protein		
25	1097	62.2	398	1	G3MSM	Ig gamma-3 chain C	A;Cross-references: 136-154, 'Q', '15-16-165, 'Q', '167-176, 'Q', '178-194, 'N', '196-197, 'D', '199-238, 'E', 240,		
26	1093	62.0	330	1	G3MSA	Ig gamma-2a chain	A;Note: this sequence has the Gimmon-1 markers, 239-Glu and 241-Met		
27	1093	62.0	469	2	S37483	Ig gamma-2a chain	R;Ponting, H.; Hilschmann, N.		
28	1090.5	61.8	335	1	G3MSA	Ig gamma-2a chain	Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976		
29	1088	61.7	393	1	G3MSAM	Ig gamma-2a chain	A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunoglobulins (Myelomprotein Nie),		

igen Primärstruktur.

A;Reference number: A91668; MUID:77070269; PMID:826475

A;Contents: myeloma protein Nie

A;Accession: B91668

A;Molecule type: protein

A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'B', 270-273

A;Note: this sequence has the Gim(17) and Gim(11) markers

R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler', Z. Physiol. Chem. 364, 713-747, 1983

A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL

A;Reference number: A91723; MUID:83289331; PMID:884994

A;Contents: myeloma protein KOL; disulfide bonds

A;Accession: A91723

A;Molecule type: protein

A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH>

A;Note: this sequence has the Gim(3) and Gim(non-1) markers

R;Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3195, 1970

A;Title: The covalent structure of a human Gamma-G-immunoglobulin. X. Intrachain disulfide bonds

A;Contents: annotation; disulfide bonds

R;Dreier, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler', Z. Physiol. Chem. 357, 1515-1540, 1976

A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin. Embromide cleavage products, and the disulfide bridges.

A;Contents: annotation; disulfide bonds

C;Genetics:

A;Gene:IGHG1

A;Cross-references: GDB:120085; OMIM:147100

A;Map position: 14q32.3-14q32.33

A;Intron: 99/1; 114/1; 224/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ or λ) chains disulfide bonded. In some cases, such as IgA and IgM, the subunits associate into larger complexes: immunoglobulin C region; immunoglobulin homology

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/domain: immunoglobulin homology <IM2>

F;20-85-206/Domain: immunoglobulin homology <IM3>

F;24-3-310/Domain: disulfide bonds; #status experimental

F;21-83-144-204, 250-308/disulfide bonds; #status experimental

F;03/03/03/disulfide bonds; interchain (to light chain) #status experimental

F;09-112/disulfide bonds; interchain (to heavy chain) #status experimental

F;180/Binding Site: Carbohydrate (Asn) (covalent) #status experimental

Query Match 90.3%; Score 152.5; DB 2; Length 377; Best Local Similarity 80.1%; Pred. No. 7.7e-103; Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

Db QY 1 ASTKGPSVFLPAPSRSKSTSGTAAGCLVYDFRFPVTSSWNNSGALTSGWHTPAVLOSS 60

Db QY 1 ASTKGPSVFLPAPSRSKSTSGTAAGCLVYDFRFPVTSSWNNSGALTSGWHTPAVLOSS 60

Db QY 61 GLYSLSSSVVTPSSSLGTGTYCICNWNHKPSNTKVDKV--..... 98

Db 61 GLYSLSSSVVTPSSSLGTGTYCICNWNHKPSNTKVDKVLEKLTKPLGDTTHCPRCPBPKSC 120

Db QY 99 -----EPKSDDKTHCPCPPAPELGGPVEFLRPPKPKOT 133

Db 121 DTPPPCPRCBPKSCDTPPPCPRCBPKSCDTPPPCPRCBPAPELIGGSPVFLFPPKPKOT 180

Db QY 134 LMISRTPEVTCVVWDVSHEDEPVKENWYDGVENAKCVPREOYNSTYVWSLTVH 193

Db 181 LMISRTPEVTCVVWDVSHEDEPVVKWYDGVENAKCVPREOYNSTYVWSLTVH 240

Db QY 194 QNWNGKEYCKVSKNALPAPIEKITSKAVQRPBVQVTLPPSDDELTNQVSLTLYRK 253

Db 241 QDWLNKEKEYCKVSKNALPAPIEKITSKAVQRPBVQVTLPPSRBEMTNQVSLTLYRK 300

Db QY 254 GFYPSDIAWESNGQPENNYKTTPVPLSSVGSPFLYSKLTVDSSRWQGNGVFCSSVMH 313

Db 301 GFYPSDIAWESNGQPENNYNTTPMLSDGSFLYSKLTVDSSRWQGNGVFCSSVMH 360

Db QY 314 ALHNHQQRSLSLSGK 330

Db 361 ALHNRFQTSLSLSGK 377

RESULT 3

A60764 121 PSVFLFPPKPKDLMISRTPEVTCVVWDVSHEDEPVKENWYDGVENAKCVPREOYN 180

181 STRYVSVLTLHOMWNGKEYCKVSKNALPAPIEKITSKAVQRPBVQVTLPPSD 240

181 STRYVSVLTLHOMWNGKEYCKVSKNALPAPIEKITSKAVQRPBVQVTLPPSD 240

241 LTKNOVSLTCLVKGFPYPSDAVEWESNGQPENNYKTTPVPLSSVGSPFLYSKLTVDSSRW 300

241 LTKNOVSLTCLVKGFPYPSDAVEWESNGQPENNYKTTPVPLSSVGSPFLYSKLTVDSSRW 300

301 QQGNVFSCSVMEALHNHYTQSLSLSPGK 330

301 QQGNVFSCSVMEALHNHYTQSLSLSPGK 330

C;Species: Homo sapiens (man)

C;Accession: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004

R;Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A;Title: A human immunoglobulin IgHg4 allele (Gmb0, b1, c3, c5, u) with an IgHg4 converted allele.

A;Reference number: A60764; MUID:99007613; PMID:2571587

A;Accession: A60764

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-377 <HUC>

A;Cross-references: UNIPROT:QBN4Y9

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>	A;Accession: A93132
Query Match 90.2%; Score 1590.5; DB 2; Length 377;	A;Molecule type: protein
Best Local Similarity 80.1%; Pred. No. 1.1e-102;	A;Residues: 238-275 <HOF>
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;	R.Hofmann, T.; Parr, D.M.
	submitted to the Atlas, March 1980
	A;Reference number: A94591
	A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
Qy 1 ASTKGPSVFPPLAPCSRSITSGGTAALGCLVKDFPPEPVTVSMNSGALTSGVHTFPAVIQSS 60	A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidation of R.Milstein, C.; Frangione, B.
Db 1 ASTKGPSVFPPLAPCSRSITSGGTAALGCLVKDFPPEPVTVSMNSGALTSGVHTFPAVIQSS 60	R.Milstein, C.; Milstein, C.; Pink, J.R.L.
Qy 61 GLYSLSVVTVSSGSGTQTYCNVKPNSNPKDKEY----- 98	Nature 221, 145-148, 1969
Db 61 GLYSLSVVTVSSGSGTQTYCNVKPNSNPKDKEY----- 98	A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G.
Qy 134 LMISRTPETCVVVDVSHEDPEVKENWYDGVEVHAKTKPREEQNSTFRVSVLVLH 193	A;Reference number: A93157; MUID:69664124; PMID:5782707
Db 181 LMISRTPETCVVVDVSHEDPEVKENWYDGVEVHAKTKPREEQNSTFRVSVLVLH 240	A;Contents: annotation; Sa, disulfide bonds
Qy 194 QNWNGKEYKCKVSNKALPPIEKTTSKAVQVPREPQVTLPSPDLTKNOVSICLVK 253	C;Genetics:
Db 241 QDWLNKEKYKCKVSNKALPPIEKTTSKAVQVPREPQVTLPSPDLTKNOVSICLVK 300	A;Gene: GDB:IGHG2
Qy 254 GFYPSDIAVEWESNGQOPENNYKTPPVLDGSFVGSFLYSLRITVDSKSRQEGNVFCSTMHE 313	A;Cross-references: GDB:119338; OMIM:147110
Db 301 GFYPSDIAVEWESNGQOPENNYKTPPVLDGSFVGSFLYSLRITVDSKSRQEGNVFCSTMHE 360	A;Map position: 1q42.33-1q42.33
Qy 314 ALHNHQQRSIISLSPGK 330	C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a superfamily: immunoglobulin C region; immunoglobulin homology <IM1>
Db 361 ALHNRFIQKSISLSPGK 377	C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;133-202/Domain: immunoglobulin homology <IM3>
RESULT 4	F;239-306/Domain: immunoglobulin homology <IM3>
G2HU	F;144/disulfide bonds: interchain (to light chain) #status experimental
19 gamma-2 chain C region - human	F;27-83, 140-200, 246-304/disulfide bonds: interchain (to heavy chain) #status experimental
;Species: Homo sapiens (man)	F;102, 103, 106, 109/disulfide bonds: interchain (covalent) #status predicted
;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004	F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
C;Accession: A93906; A92809; A90752; A9132; A92148	Query Match 88.8%; Score 1566; DB 1; Length 326;
R;Ellison, J.; Hood, L.	Best Local Similarity 89.1%; Pred. No. 4.4e-101;
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982	Matches 294; Conservative 15; Mismatches 17; Indels 4; Gaps 2;
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain core proteins. Nucleic Acids Res. 10, 1982	Qy 1 ASTKGPSVFPPLAPCSRSITSGGTAALGCLVKDFPPEPVTVSMNSGALTSGVHTFPAVIQSS 60
A;Reference number: A93906; MUID:82197621; PMID:6804948	Db 1 ASTKGPSVFPPLAPCSRSITSGGTAALGCLVKDFPPEPVTVSMNSGALTSGVHTFPAVIQSS 60
A;Molecule type: DNA	Qy 61 GLYSLSVVTVSSGSGTQTYCNVKPNSNPKDKEY----- 98
A;Residues: 1-326 <ELL>	Db 61 GLYSLSVVTVSSGSGTQTYCNVKPNSNPKDKEY----- 98
A;Cross-references: UNIPROT: P01859; GB: V00554; GB: J00230; NTID: q32759; PIDN: CAB54438.1; E	Qy 121 PSVLFPPKKPDKTLMISRTPETCVVVDVSHEDPEVKENWYDGVEVHAKTKPREEQNF 180
R;Wang, A.C.; Tung, B.; Fudenberg, H.H.	Db 117 PSVLFPPKKPDKTLMISRTPETCVVVDVSHEDPEVKENWYDGVEVHAKTKPREEQNF 176
J. Immunol. 125, 1018-1054, 1980	Qy 181 SYRWSVLTIVHVNWNKGKEYKCKVSNKALPPIEKTTSKAVQVPREPQVTLPSPRDE 240
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional comparison with IgG1. J. Biol. Chem. 257, 758-767, 1979	Db 177 SFRVVSVLTIVHVNWNKGKEYKCKVSNKALPPIEKTTSKAVQVPREPQVTLPSPRDE 236
R;Connell, G.E.; Parr, D.M.; Hofmann, T.	Qy 241 LTKNQSLTCLYKGFYSDIAVEWESNGQOPENNYKTPPVLDGSFVGSFLYSLRITVDSKSRW 300
R;Canell, J.; Biochem. 57, 758-767, 1979	Db 237 NTKNQSLTCLYKGFYSDIAVEWESNGQOPENNYKTPPVLDGSFVGSFLYSLRITVDSKSRW 296
A;Title: The amino acid sequences of the three heavy chain constant region domains of a	Qy 301 QDNVFSCSVMHEALHHHYQDSLISLSPGK 330
A;Reference number: A90752; MUID:80001357; PMID:1136060	Db 297 QDNVFSCSVMHEALHHHYQDSLISLSPGK 326
A;Contents: myeloma protein Zie	
A;Accession: A90752	
A;Molecule type: protein	
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-	RESULT 5
A;Note: this sequence has since been revised	G4HU
R;Hofmann, T.; Parr, D.M.	Ig gamma-4 chain C region - human
Mol. Immunol. 16, 923-925, 1979	C;Species: Homo sapiens (man)
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G	C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
A;Reference number: A93132; MUID:80114419; PMID:118920	C;Accession: A9933; A90219; A92150
A;Contents: Zie	R;Ellison, J.; Buxbaum, J.; Hood, L.
	DNA 1, 11-18, 1981
	A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A; Reference number: A90933; MUID:83157104; PMID:6299662  
A; Accession: A90933  
A; Molecule type: DNA  
A; Residues: 1-327 <ELL>  
A; Cross-references: UNIPROT:P01861  
A; Note: the sequence was determined from the germline gene  
R; Park, J.R.L.; Butterly, S.H.; De Vries, G.M.; Mistlein, C.  
Bloch, J. 117, 33-47, 1970  
A; Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant region  
A; Reference number: A90249; MUID:7020560; PMID:4192699  
A; Accession: A90249  
A; Molecule type: protein  
A; Residues: 1-30; 81-326 <PRN>  
A; Genetics:  
A; Gene: GDB:IGHG4  
A; Cross-references: GDB:119340; OMIM:147130  
A; Map position: 1q32.33-1q32.33  
A; Introns: 99/1; 111/1; 221/1  
A; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a heterotetramer.  
C; Superfamily: immunoglobulin C region; immunoglobulin homology  
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F; 20-85/Domain: immunoglobulin homology <IM>  
F; 99-110/Region: hinge  
F; 134-205/Domain: immunoglobulin homology <IM>  
F; 240-307/Domain: immunoglobulin homology <IM>  
F; 14/Disulfide bonds: interchain (to light chain) #status experimental  
F; 27-83/141-201,247-305/Disulfide bonds: #status predicted  
F; 106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F; 177/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 88.0%; Score 1552.5; DB 1; Length 327;  
Best Local Similarity 88.8%; Pred. No. 3.8e-100;  
Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;  
Qy 1 ASTKGPSVPLAPSSKSTSGTAAAGCLVLDYPERPVTKNSGALTSGVHTPAVLOSS 60  
Db 1 ASTKGPSVPLAPCSRSTESTAALGCLVLDYPERPVTKNSGALTSGVHTPAVLOSS 60  
Qy 61 GLYSASSVVTPPSSGLGTQYICWNHKSPTKVDKVKVEPKSCDKTHCPCPAPELGG 120  
Db 61 GLYSASSVVTPPSSGLGTQYICWNHKSPTKVDKVKVEPKSCDKTHCPCPAPELGG 117  
Qy 121 PSVFLPPPKKDITMISRTPEVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQYN 180  
Db 118 PSVFLPPPKKDITMISRTPEVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQFN 177  
Qy 181 STYRVVSLVLTQHOMWNGEYKCKVSNKALPAPKETSKAKVQPREPVYTLPSRDE 240  
Db 178 STYRVVSLVLTQHOMWNGEYKCKVSNKALPAPKETSKAKVQPREPVYTLPSQEE 237  
Qy 241 LTKNQSLTCLVKGFGPSDIAVEWESNGQPNKYITPPVLDGSFFLYSKLTVDKSRW 300  
Db 238 MTQNQSLTCLVKGFGPSDIAVEWESNGQPNKYITPPVLDGSFFLYSKLTVDKSRW 297  
Qy 301 QGNYTFSCSCTMHEALHNHYQRSLSLSPGK 330  
Db 298 QEGNTFSCCSVNHEALHNHYTOKSLSLSGK 327

RESULT 6

S9339 Ig heavy chain v region precursor - human  
C; Species: Homo sapiens (man)  
C; Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C; Accession: S69339; S72664  
R; Khamlich, A.R.; Autourier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A; Reference number: S69339; MUID:95262687; PMID:7744049  
A; Accession: S69339  
A; Status: preliminary  
A; Molecule type: mRNA

Query Match 69.5%; Score 1225; DB 2; Length 328;  
Best Local Similarity 87.1%; Pred. No. 1.8e-77;  
Matches 224; Conservative 6; Mismatches 56; Indels 6; Gaps 2;  
Qy 1 ASTKGPSVPLAPSSKSTSGTAAAGCLVLDYPERPVTKNSGALTSGVHTPAVLOSS 60  
Db 1 APKTAPSVPLAPCSRSTESTAALGCLVLDYPERPVTKNSGALTSGVHTPAVLOSS 60  
Qy 61 GLYSASSVVTPPSSGLGTQYICWNHKSPTKVDKVKVEPKSCDKTHCPCPAPELGG 120  
Db 61 GLYSASSVVTPPSSGLGTQYICWNHKSPTKVDKVKVEPKSCDKTHCPCPAPELGG 116  
Qy 121 PSVFLPPPKKDITMISRTPEVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQYN 180  
Db 117 PSVFLPPPKKDITMISRTPEVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQFN 176

Query Match 69.5%; Score 1225.5; DB 2; Length 374;  
Best Local Similarity 87.1%; Pred. No. 1.8e-77;  
Matches 230; Conservative 6; Mismatches 17; Indels 11; Gaps 2;  
Qy 78 TQTYICCNVN-----HK-PSNTKVVKRVEPKSCDKTHCPCPAPELGGPSVFL 126  
Db 111 TATYICGNVN-----HK-PSNTKVVKRVEPKSCDKTHCPCPAPELGGPSVFL 170  
Qy 127 PPKDTIMSRTPETVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQYN 185  
Db 171 PPKDTIMSRTPETVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQYN 230  
Qy 187 SVLTVLHQWNGKEYKCKVSNKALPAPKETSKAKVQPREPVYTLPSRDLTRW 246  
Db 231 SVLTVLHQWNGKEYKCKVSNKALPAPKETSKAKVQPREPVYTLPSRDLTRW 290  
Qy 247 SLTCLVKGFPSPDIAVEWESNGQPNKYITPPVLDGSFFLYSKLTVDKSRWQGNYT 305  
Db 291 SLTCLVKGFPSPDIAVEWESNGQPNKYITPPVLDGSFFLYSKLTVDKSRWQGNYT 350  
Qy 307 SC5VMEALTHNHYQRSLSLSPGK 330  
Db 351 SC5VMEALTHNHYQTSLSLSPGK 374

RESULT 7

I47159

Ig gamma 2a chain constant region - pig (fragment)

C; Species: Sus scrofa domestica (domestic pig)  
C; Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C; Accession: I47159  
R; Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A; Title: Five putative subclases of swine IgG identified from the cDNA sequences of a single transcript  
A; Reference number: I47159; MUID:95015845; PMID:7930579  
A; Accession: I47159  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 1-328 <KGK>  
A; Cross-references: EMBL:U03779; NID:9433123; PID:AAA52217.1; RID:9433124  
C; Genetics:  
A; Gene: IGG2a  
C; Superfamily: immunoglobulin C region; immunoglobulin homology <IM>  
C; Domain: immunoglobulin C region; immunoglobulin homology <IM>  
F; 133-202/Domain: immunoglobulin homology <IM>

Query Match 69.4%; Score 1225; DB 2; Length 328;  
Best Local Similarity 67.5%; Pred. No. 1.7e-77;  
Matches 224; Conservative 46; Mismatches 56; Indels 6; Gaps 2;

Qy 1 ASTKGPSVPLAPSSKSTSGTAAAGCLVLDYPERPVTKNSGALTSGVHTPAVLOSS 60  
Db 1 APKTAPSVPLAPCSRSTESTAALGCLVLDYPERPVTKNSGALTSGVHTPAVLOSS 60  
Qy 61 GLYSASSVVTPPSSGLGTQYICWNHKSPTKVDKVKVEPKSCDKTHCPCPAPELGG 120  
Db 61 GLYSASSVVTPPSSGLGTQYICWNHKSPTKVDKVKVEPKSCDKTHCPCPAPELGG 116  
Qy 121 PSVFLPPPKKDITMISRTPEVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQYN 180  
Db 117 PSVFLPPPKKDITMISRTPEVTCVWVDSHEDPEVKFNWYDGVYEVHVKTKREEQFN 176

QY 181 STYRVISVLTIVLHQNMNGKEYKCKVSKNKLPAPIEKTISKAKVOPREPQYTLPSPRDE 240  
 Db 177 STYRVISVLPPIQHQDWLNGKEFKCKVNKLPAPIEKTISKAKGQTREPOVYTLPHAE 236  
 QY 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQ - PENNYKTPPVLDVGFSFLYKSLTVDKS 298  
 Db 237 LSRSKVSICTLVIGFYPPDIDVEWQRNGQPEPENYRTTPBQQDVGTYFLYSKFSVDKA 296  
 QY 299 RWQGANVFSCSVMMHEALHNHYQORSLSLSPGK 330  
 Db 297 SWQGGGIFQCAVMHEALHNHYTOKSISKTPEK 328

RESULT 8

Ig gamma-1 chain C region - synthetic

C;Species: synthetic  
 A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
 C;Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
 C;Accession: S31866  
 R;Filipula, D.  
 A;Description: Screening method for protein-protein interactions of cloned gene products.  
 A;Reference number: S31866  
 A;Accession: S31866  
 A;Molecule type: mRNA  
 A;Residues: 1-255 <FILE>  
 C;Keywords: immunoglobulin  
 C;Cross-references: EMBL:X70421; NID:933068; PIDN:CAA49866.1; PID:933069  
 F;23-255/Region: Escherichia coli outer membrane protein A precursor

Query Match 69.3%; Score 1222; DB 4; Length 255;  
 Best local Similarity 94.6%; Pred. No. 2e-77; Matches 226; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 92 TKVDKKEVKPCKSKCQHCKTCPPAPAPIELLGGSVFLPPKPKDTLMISRTPBTVCVVVDVSH 151  
 Db 177 VVAQADVESKSCDKTHITCPCCPAPAPIELLGGSVFLPPKPKDTLMISRTPBTVCVVVDVSH 76

QY 152 EDPEVKFNWYDGVETHANKTKRREQYNSTYRVSVLTIVLHQNMNGKEYKCKVSKNKL 211  
 Db 77 EDPEVKFNWYDGVETHANKTKRREQYNSTYRVSVLTIVLHQNMNGKEYKCKVSKNKL 136

QY 212 PAPIEKTISKAKVQREPQVTLPSPRSDELTKNQSLITCLVKGFYPSDIAVEWESNGQ 271  
 Db 137 PAPIEKTISKAKGQREPQVTLPSPRSDELTKNQSLITCLVKGFYPSDIAVEWESNGQ 196

QY 272 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQGANVFSCSVMMHEALHNHYTOKSISKTPEK 330  
 Db 197 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQGANVFSCSVMMHEALHNHYTOKSISKTPEK 255

RESULT 9

Ig gamma 2b chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47160  
 R;Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3365-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single gene  
 A;Reference number: I47158; NID:95015845; PMID:7930579  
 A;Accession: I47160  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-328 <RAC>  
 A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AA52218.1; PID:9433126  
 C;Genetic:

QY 150 SHEDPEVKFNWYDGVETHANKTKRREQYNSTYRVSVLTIVLHQNMNGKEYKCKVSKNKL 209  
 Db 61 SHEDPEVKFNWYDGVETHANKTKRREQYNSTYRVSVLTIVLHQDWLNGKEFKCKVNKL 120

QY 210 ALPAPIEKTISKAKQREPQVTLPSPRSDELTKNQSLITCLVKGFYPSDIAVEWESNGQ 269  
 Db 121 ALPAPIEKTISKAKQREPQVTLPSPRSDELTKNQSLITCLVKGFYPSDIAVEWESNGQ 180

QY 270 PENNYKTPPVLDVGFSFFYKSLTVDKSRWQGANVFSCSVMMHEALHNHYQORS 323  
 Db 181 PENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGANVFSCSVMMHEALHNHYTOKSISKTPEK 234

RESULT 11

Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47158

QY 1 ASTKGGSVFPPLAPSSKSTSGTAALGCLVVDKYPBPVTVNSGALTSGTGTTPAVLOSS 60  
 Db 1 APKTAFLVPLAPCGRDTSQPNVAAGCLASSYFPEPVTVNSGALTSGTGTTPAVLOSS 60

QY 61 GLYSLSVVTPVSSSLGQTQTYICNVNHKPSNTKVKRVEPKSCDKHTCPCCPABLLGG 120  
 Db 61 GLYSLSVVTPVASSLSSKSYTCNVNHKPAVTTKVKRVGKTKPPCPICACESP---G 116

QY 121 PSVFLPPPKPDKTLMISRTPBTVCVVVDVSHEDPEVKFNWYDGVETHANKTKRREQYN 180  
 Db 117 PSVFLPPPKPDKTLMISRTPBTVCVVVDVSHQEVFOVSHVTDGVVBHTAQTRPKEQFN 176

QY 181 STYRVISVLTIVLHQNMNGKEYKCKVSKNKLPAPIEKTISKAKVOPREPQYTLPSPRDE 240  
 Db 177 STYRVISVLPPIQHQDWLNGKEFKCKVNKLPAPIEKTISKAKGQTREPOVYTLPHAE 236

QY 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQ - PENNYKTPPVLDVGFSFFLYKSLTVDKS 298  
 Db 237 LSRSKVSICTLVIGFYPPDIDVEWQRNGQPEPENYRTTPBQQDVGTYFLYSKFSVDKA 296

QY 299 RWQGANVFSCSVMMHEALHNHYQORSLSLSPGK 330  
 Db 297 SWQGGGIFQCAVMHEALHNHYTOKSISKTPEK 328

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A;Cross-references: EMBL:U03778; NID:9433121; PIDN:AA52216.1; PID:9433122  
A;Reference number: 147158; MUID:9501845; PMID:7930579  
A;Gene: IGG1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM>  
F;133-202/Domain: immunoglobulin homology <IM>  
Query Match 67.6%; Score 1193; DB 2; Length 328;  
Best Local Similarity 67.2%; Pred. No. 2.7e-75;  
Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;  
QY 1 ASTKGKSVFPLAPSSSTSGCTTAALGCLVKDQFPRFVTVWSNGALTSGVHTPAVLQSS 60  
1 APKTAVPSVYPLAPCGRDVGSGNVNALVALQPSL 60  
Db 61 GLYSLSGSWVTPASSLSSKSYTCNTNHPARTTKVDRV--GIGRPFCTCPCGCE-VAG 116  
61 GLYSLSGSWVTPASSLSSKSYTCNTNHPARTTKVDRV--GIGRPFCTCPCGCE-VAG 116  
QY 121 PSVFIFLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVUDGVGVHVNWKTKREEQYN 180  
117 PSVFFLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVUDGVGVHVNWKTKREEQYN 176  
Db 181 STYRVSVLVLQHONWNGKEYKCKVSKNSNKALPAPIKETISKAKVQPREPOVYTLPSSRDE 240  
QY 177 STYRVSVLVLQHONWNGKEYKCKVSKNSNKALPAPIKETISKAKVQPREPOVYTLPSSRDE 236  
Db 241 LTRKQSLTCLVKGFPDSIADVEMNGQ - PENNYKTPVLDVGSGFPLFLYSKLTDKS 298  
QY 237 LSRSKVTLCTLVIGFPPDHFVWEMNGQEPENTYRTTPQDQYTGFLYSKLAQDKA 296  
Db 299 RWOQGNTVFSCSVMHHEALTHNHYQORSLSLSPGK 330  
QY 297 RWDHGDKFKECAVMHEALTHNHYQOKSIKTIQCK 328

RESULT 12

GHRB  
Ig gamma chain C region - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text\_change 09-Jul-2004  
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161  
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot  
A;Reference number: A91749; MUID:84030930; PMID:6313520  
A;Molecule type: mRNA  
A;Residues: 1-323 <BER>  
A;Cross-references: UNIPROT:PO1870  
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
R;Protein: D.M.; Mole: L.E.  
Biochem. J. 151, 337-349, 1975  
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulins. I. The gamma 3 chain constant region - pig (fragment)  
A;Reference number: A90290  
A;Molecule type: protein  
A;Accession: A93928  
A;Molecule type: mRNA  
A;Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
A;Cross-references: GB:MG6426; NID:916511; PIDN:AAA312891; PID:9165112  
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
A;Reference number: A93928; MUID:83299917; PMID:6193512  
R;Hill, R.I.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.; Molle, R.G.; Porter, R.R.; Frueh, R.J.; Jackson, S.A.; Moore, L.E.; Porter, R.R.; Biochem. J. 116, 249-259, 1970  
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C  
A;Reference number: A90245; MUID:70110015; PMID:5461106  
A;Accession: A9245  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03781; NID:9433127;  
A;Genetics:  
C;Genetic:  
A;Gene: IgG3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM>  
F;133-202/Domain: immunoglobulin homology <IM>  
Query Match 67.6%; Score 1193; DB 2; Length 328;  
Best Local Similarity 67.2%; Pred. No. 2.7e-75;  
Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;  
QY 4 KGPSVPLAPSSKSTSGGTMALGCLVKDQFPRFVTVWSNGALTSGVHTPAVLQSS 63  
Db 4 KAPSVPFLAPCGDPSPSSTVTLGCLVKGYLPEPTVTVNGTLLNGVRTPSPVRSQGLY 63  
QY 64 SLSSVTVRSASSLGQTQYICNNRKPNSNITKVDKKEVPEKGSCKDTKTCPPCPAPENLGGPSV 123  
Db 64 SLSSVTVRSASSLGQTQYICNNRKPNSNITKVDKKEVPEKGSCKDTKTCPPCPAPENLGGPSV 116  
Db 124 FLFPLPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVUDGVGVHVNWKTKREEQNSTY 183  
Db 117 FIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVUDGVGVHVNWKTKREEQNSTY 176  
Db 184 RVSVLTVLHQHONWNGKEYKCKVSKNSNKALPAPIKETISKAKVQPREPOVYTLPSSRDELT 243  
Db 177 RVSVLTVLHQHONWNGKEYKCKVSKNSNKALPAPIKETISKAKVQPREPOVYTLPSSRDELT 236  
QY 244 NOVSLTCLVKGFPDSIADVEMNGQEPENNYKTPVLDVGSGFPLFLYSKLTDKS 303  
Db 237 RSVSLTOMINGFPYPSDISVWEKNGRAEDNYKTPAVLBDGSPYFLYKLUSVTPSEWQRG 296  
QY 304 NVEFSVVMHEALTHNHYQORSLSLSPGK 330  
Db 297 DVFTCSVVMHEALTHNHYQOKSIKTIQCK 323

RESULT 13

I47161  
Ig gamma 3 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic Pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47161  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 133, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A;Reference number: I47158; MUID:9501845; PMID:7930579  
A;Accession: I47161  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03781; NID:9433127;  
A;Genetics:  
C;Genetic:  
A;Gene: IgG3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM>  
F;133-202/Domain: immunoglobulin homology <IM>



Db 202 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
202 GLYSLSSWVTVPAASGAOPICNTAHPASSTKVKRVEPGCPDPCKH-C-RCPPELPGG 260  
Qy 121 PSVFIFPPKDKDTMISRTPEVTCVVVDVSHEDPEVKENNYDGVVEVNVTKREEQYN 180  
121 ||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 261 PSVFIFPPKDKDTLTSQTGTEBVCVNVDVQDPEVQFSMVPVUDNVEVRTARTKREEQFN 320  
261 ||||:|||||:|||||:|||||:|||||:|||||:  
Qy 181 STYRVVSLVTLHOMMNGKEYCKVUSNKALPAPTEKTISAKVOPREPOVYTIPPSRDE 240  
181 ||||:|||||:|||||:|||||:|||||:|||||:  
Db 321 STFRVWSALPIQHODWTGGKFCKVHNREALPAPIVRTISRTKGAREPOVYVLAPOQE 380  
321 ||||:|||||:|||||:|||||:  
Qy 241 LTKNOVSLSLCLVKGYPSTDAVEWESNGQP-ENYKTTTPVLDVGSGSFLLYSKLTVDKS 298  
241 ||||:|||||:|||||:|||||:  
Db 381 LSKSTLUSVTCVLTGFYPDYIAVEWQKNGQBESEDKYGTTSQDADGSYFLYSLRVDKN 440  
381 ||||:|||||:|||||:  
Qy 299 RWQGSNFSCSVMMHEALHNHYQQRSLSLSPCK 330  
299 ||||:|||||:  
Db 441 SWQEGDTIACVVMHEALHNHYTQKGISKPKX 472  
441 ||||:|||||:

Search completed: June 7, 2005, 09:02:33  
Job time : 35.7668 secs



RA	Gall W.E.; Edelman G.M.;	FT DOMAIN 111 223 CH2.
RT	"The covalent structure of a human gamma G-immunoglobulin. X.	FT DOMAIN 224 330 CH3.
RT	Intrachain disulfide bonds.";	FT DISULFID 27 83
RL	Biochemistry 9:3188-3196(1970).	FT DISULFID 103 103 Interchain (with light chain).
RN	{7}	FT DISULFID 109 109 Interchain (with heavy chain).
RP	DISULFIDE BONDS.	FT DISULFID 112 112 Interchain (with heavy chain).
RX		FT DISULFID 144 204 N-linked (GlcNAc, .').
RA	MEDLINE=77070267; PubMed=1002129;	FT DISULFID 250 308 K->R (in GlcNAc marker).
RT	Dreicer L., Schwarz J., Reichel W., Hilschmann N.;	FT CARBOHYD 180 180 /FTid=VAR_003886.
RT	"Rule of antibody structure. The primary structure of a monoclonal	FT VARIANT 97 97 D->E (in GlcNAc marker).
RT	IgG1 immunoglobulin (myeloma protein Nie), I: purification and	FT VARIANT 239 239 L->M (in GlcNAc marker).
RT	characterization of the protein, the L- and H-chains, the cyanogen	FT VARIANT 241 241 /FTid=VAR_003887.
RT	bromide cleavage products, and the disulfide bridges.";	FT VARIANT 26 33 /FTid=VAR_003888.
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).	
RN	[8]	
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).	
RX		
RA	Medline=91208100; PubMed=7236608;	
RA	Deisenhofer J.;	
RT	"Crystallographic refinement and atomic models of a human Fc fragment	
RT	and its complex with fragment B of protein A from <i>Staphylococcus</i>	
RT	aurae at 2.9- and 2.8-A resolution.";	
RL	Biochemistry 20:2351-2370(1981).	
CC	-1- MISCELLANEOUS: Nie has the Glm(17) allotypic marker, 97-K, and the	
CC	GlM(1) markers, 239-D and 241-L, KOL and EU sequences have the	
CC	GlM(3) marker and the GlM (non-1) markers	
CC	-1- MISCELLANEOUS: Nie also differs in the amidation states of 35,	
CC	116, 198, 269 and 272.	
CC	-1- MISCELLANEOUS: EU also differs in the amidation states of residues	
CC	155, 166, 177, 195, 198, 269, and 272 and in the order of residues	
CC	268-272.	
CC	-1- MISCELLANEOUS: KOL also differs in the amidation states of	
CC	residues 198, 267 and 272.	
CC		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	the European Bioinformatics Institute. There are no restrictions on its	
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CC		
EMBL	J00228; AAC85257.1; ALT_INIT.	
DR		
DR	PIR: A94433; GHHU.	
DR	PDB; 1A07; X-ray; H=1-103.	FT TURN 102 103
DR	PDB; 1D5B; X-ray; B/H=1-101.	FT STRAND 122 126
DR	PDB; 1D5I; X-ray; H=1-101.	FT HELIX 130 134
DR	PDB; 1D6V; X-ray; H=1-101.	FT TURN 136 137
DR	PDB; 1DN2; X-ray; A/B=120-326.	FT STRAND 50 52
DR	PDB; 1E4K; X-ray; A/B=106-329.	FT TURN 57 58
DR	PDB; 1FC1; X-ray; A/B=106-329.	FT STRAND 59 61
DR	PDB; 1FC2; X-ray; D=106-329.	FT STRAND 62 71
DR	PDB; 1FCC; X-ray; A=121-326.	FT HELIX 73 75
DR	PDB; 1HZH; X-ray; H/K=1-330.	FT TURN 76 78
DR	PDB; 1I7Z; X-ray; B/D=1-103.	FT STRAND 82 87
DR	PDB; 1IIS; X-ray; A/B=107-330.	FT TURN 88 91
DR	PDB; 1L6X; X-ray; A=120-326.	FT STRAND 92 97
DR	PDB; 1OQX; X-ray; A/B=119-330.	FT TURN 103 126
DR	PDB; 2RCS; X-ray; H=1-103.	FT STRAND 136 137
DR	GeneID: 5525; HGNC: IGHG1.	FT STRAND 141 149
MM	147100:-	FT STRAND 157 162
DR	GO; GO:0005624; C:membrane fraction; NAS.	FT STRAND 163 164
GO	GO; GO:0003823; F:antigen binding; TAS.	FT STRAND 165 167
GO	GO; GO:0006955; P:immune response; NAS.	FT STRAND 171 172
KW	InterPro; IPR00110; Ig-like.	FT STRAND 176 177
DR	InterPro; IPR003006; Ig_MHC.	FT TURN 179 180
PFam	PF00047; 19; 3.	FT STRAND 183 190
DR	PROSITE; PS50355; Ig_LIKE; 3.	FT HELIX 193 197
GO	GO; GO:0003823; F:antigen binding; TAS.	FT TURN 198 199
GO	GO; GO:0006955; P:immune response; NAS.	FT STRAND 202 207
KW	Immunoglobulin C region; Immunoglobulin domain.	FT TURN 209 210
FT	NON_TER	FT STRAND 215 219
DOMAIN	1	FT STRAND 227 227
DOMAIN	1	FT STRAND 230 234
DOMAIN	1	FT STRAND 238 242
DOMAIN	1	FT STRAND 245 256
DOMAIN	1	FT STRAND 261 266
DOMAIN	1	FT TURN 267 268
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DOMAIN	1	FT STRAND 274 276
DOMAIN	1	FT STRAND 280 281
DOMAIN	1	FT TURN 283 284
DOMAIN	1	FT STRAND 287 296
DOMAIN	1	FT HELIX 297 301
DOMAIN	1	FT TURN 302 303
DOMAIN	1	FT STRAND 306 311
DOMAIN	1	FT TURN 313 314
DOMAIN	1	FT HELIX 316 318
DOMAIN	1	FT STRAND 319 324
Db	SEQUENCE 330 AA;	FT SEQUENCE 330 AA; 36106 MN; 3770EE106C2FA33D CRC64;
Qy	Query Match 98.0%; Score 1721; DB 1; Length 330;	
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
1 ASTKGPSVFLAPSSKSTGCGTAAGLGCLVYFRRPVTVWSWNNSGALTSGTVAFLLOSS 60		
1 ASTKGPSVFLAPSSKSTGCGTAAGLGCLVYFRRPVTVWSWNNSGALTSGTVAFLLOSS 60		

QY	61	GLYSLSVVTVVSSSLGGTQTYCNWHAPESTKDKKKTEPKSDKTHCPCPAPBLGG	120	DR SMART; SNO0406; IGv; 1.
Db	61	GLYSLSVVTVVSSSLGGTQTYCNWHAPESTKDKKKTEPKSDKTHCPCPAPBLGG	120	DR PROSITE; PS0035; IG_LIKE; UNKNOWN_2.
QY	121	PSVFLFPKPDKDTMISRTPEVTVVVDVSHEDPEVKFNWYDGVEVHNATKPRBEQYN	180	DR DR KW Hypothetical protein.
Db	121	PSVFLFPKPDKDTMISRTPEVTVVVDVSHEDPEVKFNWYDGVEVHNATKPRBEQYN	180	DR DR KW Hypothetical protein.
QY	181	STYRVSVLTVLHQNMNGKEYKCKVSKNKKALPAPEKTIKAKVQPREPOVYTLPSRDE	240	DR DR KW Hypothetical protein.
Db	181	STYRVSVLTVLHQNMNGKEYKCKVSKNKKALPAPEKTIKAKVQPREPOVYTLPSRDE	240	DR DR KW Hypothetical protein.
QY	241	LTKNOVSITCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDVGSPFLYSLKUTVDSKRW	300	DR DR KW Hypothetical protein.
Db	241	LTKNOVSITCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDVGSPFLYSLKUTVDSKRW	300	DR DR KW Hypothetical protein.
QY	301	QQGNVFSCSVMHEALTHYHQQSLSLSPKG	330	DR DR KW Hypothetical protein.
Db	301	QQGNVFSCSVMHEALTHYHQQSLSLSPKG	330	DR DR KW Hypothetical protein.
<b>RESULT 2</b>				
RP	06GMX6	PRELIMINARY;	PRT;	465 AA.
ID	06GMX6			
AC	06GMX6;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soakes M.B., Bonaldo M.F., Casavant T.L., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Peters G.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.;			
RC	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RC	[2]			
<b>RESULT 3</b>				
RP	07ZPFS	PRELIMINARY;	PRT;	469 AA.
ID	07ZPFS			
AC	07ZPFS;			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DE	IGGI protein.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soakes M.B., Bonaldo M.F., Casavant T.L., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Peters G.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.;			
RC	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RC	Strainsberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ database.			
RL	EMLB; BC073766; AAH73766.1; -.			
DR	InterPro; IPR03599; Ig-like.			
DR	InterPro; IPR03599; Ig-like.			
DR	InterPro; IPR03599; Ig-cl.			
DR	InterPro; IPR03006; Ig-MHC.			
DR	InterPro; IPR03596; Ig-v.			
DR	PFam; PF07654; Cl-set; 3.			
DR	SMART; SW00409; Ig; 2.			
DR	SMART; SW00407; Ig; 3.			
RP	SEQUENCE FROM N.A.			

RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051328; ARN51328\_1; -.  
DR InterPro; IPR07110; Ig-like.  
DR InterPro; IPR03597; Ig cl.  
DR InterPro; IPR03006; Ig MHC.  
DR InterPro; IPR03596; Ig v.  
DR Pfam; PF07654; Cl-set; 3.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00390; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 469 AA; 5195 MW; C8D5BE12BAAF795C CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;  
Best Local Similarity 97.9%; Pred. No. 4\_5e-118; Mismatches 3; Indels 0; Gaps 0;  
Matches 323; Conservative 3; MisMatches 4; InDelS 0; Gaps 0;

Qy 1 ASTKCPSPVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSALTSGVHTFPVLOSS 60  
Db 140 ASTKCPSPVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSALTSGVHTFPVLOSS 199

Qy 61 GLYSLSVVTVPPSSSLGTQTYICVNHHKPSNTKDKVKEVSKCDKTHTCPCCPAPELGG 120  
Db 200 GLYSLSVVTVPPSSSLGTQTYICVNHHKPSNTKDKVKEVSKCDKTHTCPCCPAPELGG 259

Qy 121 PSVFLPPPKDTLMISRTEPVTCVWVDVSHEDPEVKFNWYDGVEVHNVKTKREEQN 180  
Db 201 GLYSLSVVTVPPSSSLGTQTYICVNHHKPSNTKDKVKEVSKCDKTHTCPCCPAPELGG 259

Qy 260 PSVFLPPPKDTLMISRTEPVTCVWVDVSHEDPEVKFNWYDGVEVHNVKTKREEQN 319

Qy 181 STYRVVSVTTLHOMMNGKEYKCKVSNKALPAPIEKTISAKVQPREPOVYTLPPSDE 240  
Db 320 STYRVVSVTTLHQDWLNGKEYKCKVSNKALPAPIEKTISAKQPREPOVYTLPPSDE 379

Qy 241 LTQKQVSLTCLVKGRPSDAAVEWNSNGOPENNYKTPPVLDSGSFPLYSKLTVDKSRW 300  
Db 380 LTQKQVSLTCLVKGRPSDAAVEWNSNGOPENNYKTPPVLDSGSFPLYSKLTVDKSRW 439

Qy 301 QQGNVFSCSVNHEALHNHYQKSLSLSPK 330  
Db 440 QQGNVFSCSVNHEALHNHYQKSLSLSPK 469

RESULT 4

Q6PQA4 PRELIMINARY; PRT; 470 AA.

ID Q6PQA4 DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Homidae; Homo. [1]  
OX NCBI\_TaxID=9606;  
RN RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S., Rodriguez A.C., Grifwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzwinowski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]

RA SEQUENCE FROM N.A.  
RA TISSUE=Primary B-Cells;  
RA Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011874; ARN11874\_1; -.  
DR HSSP; P01861; IgA.  
DR InterPro; IPR03597; Ig-like.  
DR InterPro; IPR07110; Ig cl.  
DR InterPro; IPR03597; Ig cl.  
DR InterPro; IPR03066; Ig\_MHC.  
DR InterPro; IPR03586; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; Igcl; 3.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00390; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 4\_5e-118; Mismatches 3; Conservative 3; MisMatches 4; InDelS 0; Gaps 0; Matches 323; Conservative 3; MisMatches 4; InDelS 0; Gaps 0;

Qy 1 ASTKCPSPVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSALTSGVHTFPVLOSS 60  
Db 141 ASTKCPSPVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSALTSGVHTFPVLOSS 200

Qy 61 GLYSLSVVTVPPSSSLGTQTYICVNHHKPSNTKDKVKEVSKCDKTHTCPCCPAPELGG 120  
Db 201 GLYSLSVVTVPPSSSLGTQTYICVNHHKPSNTKDKVKEVSKCDKTHTCPCCPAPELGG 260

Qy 121 PSVFLPPPKDTLMISRTEPVTCVWVDVSHEDPEVKFNWYDGVEVHNVKTKREEQN 180  
Db 202 PSVFLPPPKDTLMISRTEPVTCVWVDVSHEDPEVKFNWYDGVEVHNVKTKREEQN 320

Qy 181 STYRVVSVTTLHOMMNGKEYKCKVSNKALPAPIEKTISAKVQPREPOVYTLPPSDE 240  
Db 321 STYRVVSVTTLHQDWLNGKEYKCKVSNKALPAPIEKTISAKQPREPOVYTLPPSDE 380

Qy 241 LTQKQVSLTCLVKGRPSDAAVEWNSNGOPENNYKTPPVLDSGSFPLYSKLTVDKSRW 300  
Db 381 LTQKQVSLTCLVKGRPSDAAVEWNSNGOPENNYKTPPVLDSGSFPLYSKLTVDKSRW 440

Qy 301 QQGNVFSCSVNHEALHNHYQKSLSLSPK 330  
Db 441 QQGNVFSCSVNHEALHNHYQKSLSLSPK 470

RESULT 5

Q7Z5M1 PRELIMINARY; PRT; 470 AA.

ID Q7Z5M1 AC Q7Z5M1; DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Homidae; Homo. [1]  
OX NCBI\_TaxID=9606;  
RN RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;





DR PROSITE; PS05035; IG\_LIKE; 4.  
 DR PROSITE; PS02920; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 466 AA; 50853 MW; 53EB0CDE81076E CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 466;  
 Best Local Similarity 97.6%; Pred. No. 7.5e-118;  
 Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 9

QY 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVANGALTSGTFRTPAVLOSS 60  
 DR 143 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVANGALTSGTFRTPAVLOSS 60  
 Db 137 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVANGALTSGTFRTPAVLOSS 195  
 QY 61 GLYSLSVVTVPSSGGTQTYICINWNHKPSNTKVDRKEVKPSCKHTCPCPAPBLLGG 120  
 DR 197 GLYSLSVVTVPSSGGTQTYICINWNHKPSNTKVDRKEVKPSCKHTCPCPAPBLLGG 256  
 QY 121 PSVFELPPPKDUTMISRTPEVTCVWVDVSHEDEPVFKENMYDGVYEVHNKTKEPEQYN 180  
 DR 257 PSVFELPPPKDUTMISRTPEVTCVWVDVSHEDEPVFKENMYDGVYEVHNKTKEPEQYN 316  
 QY 181 STYRVSVLTVLHQMWNGKEYCKVSKNKLAPAPIEKTSKAKVOPREPOVYLPSRDE 240  
 DR 317 STYRVSVLTVLHQMWNGKEYCKVSKNKLAPAPIEKTSKAKGQPREGQVYLPSRDE 376  
 QY 241 LTKNQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPLSDGSFFLYSKLTVDKSRW 300  
 DR 377 LTKNQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPLSDGSFFLYSKLTVDKSRW 436  
 AC 301 QGNQFSCSYMEHALHNHYQRSLSLSPGK 330  
 QY 437 QGNQFSCSYMEHALHNHYQRSLSLSPGK 466

RESULT 9

ID Q6N089 PRELIMINARY; PRT; 472 AA.  
 AC Q6N089; PRELIMINARY; PRT; 472 AA.  
 DT 05-JUL-2004 ('tREMBirel. 27, Last sequence update')  
 DE Hypothetical protein DKF2p686p15220;  
 GN Name=DKF2p686p15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] NCBI\_TaxId=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=2388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Degege J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Louquillo N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarante P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Saliska R., Smalius D.E., Schneich A., Schein J.E., Jones S.J., Mazar M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 DR InterPro; IPR03599; IG\_LIKE; 3.  
 DR InterPro; IPR00110; IG\_LIKE.  
 DR InterPro; IPR03597; IG\_CL.  
 DR InterPro; IPR003005; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; CL\_SET; 3.  
 DR SMART; SM00009; IG; 2.  
 DR SMART; SM00407; IGC; 3.  
 DR SMART; SM00406; IG\_MHC.  
 DR PROSITE; PS05035; IG\_LIKE; 4.  
 DR PROSITE; PS02920; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D00460279 CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 472;  
 Best Local Similarity 97.6%; Pred. No. 7.6e-118;  
 Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 10

ID Q6P055 PRELIMINARY; PRT; 473 AA.  
 AC Q6P055; PRELIMINARY; PRT; 473 AA.  
 DT 05-JUL-2004 ('tREMBirel. 27, Last sequence update')  
 DT 05-JUL-2004 ('tREMBirel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] NCBI\_TaxId=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=2388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Degege J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Louquillo N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarante P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Saliska R., Smalius D.E., Schneich A., Schein J.E., Jones S.J., Mazar M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 DR InterPro; IPR03599; IG\_LIKE; 3.  
 DR InterPro; IPR00110; IG\_LIKE.  
 DR InterPro; IPR03597; IG\_CL.  
 DR InterPro; IPR003005; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.

RESULT 11

ID Q6P055 PRELIMINARY; PRT; 473 AA.  
 AC Q6P055; PRELIMINARY; PRT; 473 AA.  
 DT 05-JUL-2004 ('tREMBirel. 27, Last sequence update')  
 DT 05-JUL-2004 ('tREMBirel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] NCBI\_TaxId=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=2388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Degege J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Louquillo N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarante P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Saliska R., Smalius D.E., Schneich A., Schein J.E., Jones S.J., Mazar M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 DR InterPro; IPR03599; IG\_LIKE; 3.  
 DR InterPro; IPR00110; IG\_LIKE.  
 DR InterPro; IPR03597; IG\_CL.  
 DR InterPro; IPR003005; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.

DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SN00409; Ig; 2; 3.  
 DR SMART; SN00407; Ig<sub>1</sub>; 3.  
 DR SMART; SN00406; Ig<sub>v</sub>; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 4.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_2.  
 KW HYPothetical protein.  
 SQ SEQUENCE 473 AA; 5144 MW; 9816D56A7129B57 CRC64;  
 Query Match 97.8%; Score 1725; DB 2; Length 473;  
 Best Local Similarity 97.6%; Pred. No. 9e-118; Indels 5; Gaps 0;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLAPSSKSTSGGTAAALGCLVYDFPERPVWSNSGALTSGVHTPAVLOSS 60  
 Db 144 ASTKGPSVFLAPSSKSTSGGTAAALGCLVYDFPERPVWSNSGALTSGVHTPAVLOSS 203  
 Qy 61 GLYSLSVVTPSSSLGTQTYICNNHKSNTKDKKKVEKSCDKTHCPPCPAPELGG 120  
 Db 204 GLYSLSVVTPSSSLGTQTYICNNHKSNTKDKKKVEKSCDKTHCPPCPAPELGG 263  
 Qy 121 PSVFLFPPKDKDTMISRTPEVTCTVVDVSHEDPEVKENWYDGVVEHNVKTKRREEQN 180  
 Db 264 PSVFLFPPKDKDTMISRTPEVTCTVNDVSHEDPEVKENWYDGVVEHNVKTKRREEQN 323  
 Qy 241 LTKNQVSITCLVKGYPSDIAVENESNGOPENNKTTPVLDGSFPLYSKLTUDKSRW 300  
 Db 384 LTKNQVSITCLVKGYPSDIAVENESNGOPENNKTTPVLDGSFPLYSKLTUDKSRW 443  
 Qy 301 QQGNVFSCSYMHAELNHYQORSLSLSPK 330  
 Db 324 STYRVSVLTVLHQDWLNGKEYKCKVSKNKLPAIPEKTIKAKGQPREGOVTLLPSDE 383  
 Qy 444 QQGNVFSCSYMHAEGLHNHYQKSLSLSPK 473  
 RESULT 11  
 ID O6M2Q6 PRELIMINARY; PRT; 475 AA.  
 AC O6M2Q6;  
 DT 05-JUL-2004 (Tremblel. 27, Created)  
 DT 05-JUL-2004 (Tremblel. 27, Last sequence update)  
 DE Hypothetical protein DKFZp686G11190.  
 GN Name=DKFZp686G11190;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Robo G., Han M., Wiemann S., Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL; BX404947; CAB45776.1; -.  
 DR InterPro; IPR03599; Ig.  
 RC TISSUE=Human esophagus tumor;  
 RA The German Human cDNA Consortium;  
 RA Laber J., Bair A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Ham M., Wiemann S., Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 RL BX404947; CAB45772.1; -.  
 DR HSSP; P01861; IADQ;  
 DR InterPro; IPR03599; Ig.  
 DR InterPro; IPR07110; Ig-like.  
 DR InterPro; IPR03597; Ig\_c1.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR00306; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003595; Ig\_MHC.  
 DR InterPro; IPR003595; Ig\_MHC.  
 DR InterPro; IPR003595; Ig\_MHC.  
 DR InterPro; IPR003595; Ig\_MHC.  
 DR SMART; SN00409; Ig<sub>1</sub>; 3.  
 DR SMART; SN00407; Ig<sub>1</sub>; 3.  
 DR SMART; SN00406; Ig<sub>v</sub>; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 4.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_2.  
 KW HYPothetical protein.  
 SQ SEQUENCE 475 AA; 52043 MW; B7EAB25FA26F4B8E CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 480;  
 Best Local Similarity 97.6%; Pred. No. 9.2e-118; Indels 5; Gaps 0;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLAPSSKSTSGGTAAALGCLVYDFPERPVWSNSGALTSGVHTPAVLOSS 60  
 Db 146 ASTKGPSVFLAPSSKSTSGGTAAALGCLVYDFPERPVWSNSGALTSGVHTPAVLOSS 205  
 Qy 61 GLYSLSVVTPSSSLGTQTYICNNHKSNTKDKKKVEKSCDKTHCPPCPAPELGG 120  
 Db 206 GLYSLSVVTPSSSLGTQTYICNNHKSNTKDKKKVEKSCDKTHCPPCPAPELGG 265  
 Qy 121 PSVFLFPPKDKDTMISRTPEVTCTVVDVSHEDPEVKENWYDGVVEHNVKTKRREEQN 180  
 Db 266 PSVFLFPPKDKDTMISRTPEVTCTVVDVSHEDPEVKENWYDGVVEHNVKTKRREEQN 325  
 Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSKNKLPAIPEKTIKAKGQPREGOVTLLPSDE 240  
 Db 326 STYRVSVLTVLHQDWLNGKEYKCKVSKNKLPAIPEKTIKAKGQPREGOVTLLPSDE 385  
 Db 386 LTKNQVSITCLVKGYPSDIAVENESNGOPENNKTTPVLDGSFPLYSKLTUDKSRW 300  
 Qy 301 QQGNVFSCSYMHAEGLHNHYQKSLSLSPK 330  
 Db 446 QQGNVFSCSYMHAEGLHNHYQKSLSLSPK 475  
 RESULT 12  
 ID O6N94 PRELIMINARY; PRT; 480 AA.  
 AC O6N94;  
 DT 05-JUL-2004 (Tremblel. 27, Created)  
 DT 05-JUL-2004 (Tremblel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686G01196.  
 GN Name=DKFZp686G01196;  
 OS Homo sapiens (Human).  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Robo G., Han M., Wiemann S., Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL; BX404622; CAB45776.1; -.  
 DR HSSP; P01861; IADQ;  
 DR InterPro; IPR03599; Ig.  
 DR InterPro; IPR07110; Ig-like.  
 DR InterPro; IPR03597; Ig\_c1.  
 DR InterPro; IPR00306; Ig\_MHC.  
 DR InterPro; IPR03595; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SN00409; Ig<sub>1</sub>; 3.  
 DR SMART; SN00407; Ig<sub>1</sub>; 3.  
 DR SMART; SN00406; Ig<sub>v</sub>; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 4.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_2.  
 KW HYPothetical protein.  
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35ABC18 CRC64;

Qy	61 GLYSLSSSVWVTPSSSLGTOYICVNHNKPSNTKDKVKVERPKSCDKHTCPCPAPELGG	120	Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Db	211 GLYSLSSSVWVTPSSSLGTOYICVNHNKPSNTKDKVKVERPKSCDKHTCPCPAPELGG	270	Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Qy	121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNKTKREEQN	180	Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Db	271 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNKTKREEQN	330	Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240	Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Db	331 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	390	Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
RESULT 13					
Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300	Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Db	391 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	450	Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330	Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Db	451 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	480	Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
RESULT 14					
Qy	61 GLYSLSSSVWVTPSSSLGTOYICVNHNKPSNTKDKVKVERPKSCDKHTCPCPAPELGG	120	Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Ac	Q6IN097; PRELIMINARY; PRT; 481 AA.		Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Dt	05-JUL-2004 (TREMBREL. 27, Created)		Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Dt	05-JUL-2004 (TREMBREL. 27, Last annotation update)		Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
De	Hypothetical protein DKFZp686H20196.		Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Gn	Name=DKFZp686H20196;		Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
Os	Homo sapiens (Human).		Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Oc	OC		Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Rn	NCBI_TaxID=9606;		Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Rp	SEQUENCE FROM N.A.		Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Rc	TISSUE=Human rectum tumor;		Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Ra	Bloescher H., Boecker M., Meves H.W., Weil B., Amid C., Osanger A.,		Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
Ra	Fobo G., Han M., Wielmann S.; to the EMBL/GenBank/DDBJ databases.		Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Rl	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Dr	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Ox	NCBI_TAXID=9606;		Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Rn	[1]		Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Rp	SEQUENCE FROM N.A.		Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
Rc	TISSUE=Human esophagus tumor;		Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Rg	The German Human cDNA Consortium;		Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Ra	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,		Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Ra	Fobo G., Han M., Wielmann S.; to the EMBL/GenBank/DDBJ databases.		Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Rl	Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.		Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Dr	HSSP; P01857; IgH.		Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
Dr	InterPro; IPR003597; Ig_V.		Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Dr	InterPro; IPR003599; Ig.		Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Dr	InterPro; IPR007110; Ig-like.		Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Dr	InterPro; IPR003597; Ig_C1.		Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Dr	SMART; SN00407; Ig_C1.		Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Dr	SMART; SN00405; Ig_V.		Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
Dr	PROSITE; PS50335; Ig_LIKE; 4.		Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Dr	PROSITE; PS00290; Ig_MHC; UNKNOWN_2.		Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Kw	Hypothetical protein.		Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Sq	SEQUENCE 482 AA; MW: 52852 CRC64;		Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Query Match 97.8%; Score 1725; DB 2; Length 482;					
Matches	Best Local Similarity 97.6%; Pred. No. 9.2e-118; Mismatches 3; Missmatches 5; Indels 0; Gaps 0;		Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240
Qy	1 ASTKGPSVFLAPSSKSTSGATAALGCLVQDYFPEVTVSNSGALTSGWHTFPAVLOSS	60	Db	332 STYRVSVLTULHQDWLNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	391
Db	152 ASTKGPSVFLAPSSKSTSGATAALGCLVQDYFPEVTVSNSGALTSGWHTFPAVLOSS	211	Qy	241 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	300
Qy	61 GLYSLSSSVWVTPSSSLGTOYICVNHNKPSNTKDKVKVERPKSCDKHTCPCPAPELGG	120	Db	392 LTNOQVSLTCLVKGKFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFLISKLTVDKSRW	451
Db	212 GLYSLSSSVWVTPSSSLGTOYICVNHNKPSNTKDKVKVERPKSCDKHTCPCPAPELGG	271	Qy	301 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	330
Qy	121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNKTKREEQN	180	Db	452 QQGNVFSCSYNMHEALTHNHYQORSLSLSPGK	481
Db	272 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNKTKREEQN	331	Qy	181 STYRVSVLTULHQNMNGKEYKCKVSNKALPAPIEKTSKAKVOPREPOVYTLPSRDE	240

RESULT 15  
 Q61096 PRELIMINARY; PRT; 466 AA.  
 ID Q61096;  
 AC DT 05-JUL-2004 (TREMBREL; 27, Created)  
 DT 05-JUL-2004 (TREMBREL; 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBREL; 27, Last annotation update)  
 DE Hypothetical protein DKrZp686115196.  
 GN Name=DKrZp686115196;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TAXID=9606;  
 RN [1]  
 RP TISSUE=Human esophagus tumor;  
 RG The German Human cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Robo G., Han M., Wiemann S.; Submitted (AUG 2003) to the EMBL/GenBank/DDBJ databases.  
 RL DR EMBL; BI640620; CAB45774.1; -.  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-cl.  
 DR InterPro; IPR003597; Ig\_MHC.  
 DR InterPro; IPR003006; Ig\_V.  
 DR Pfam; PF07654; Cl-Ser; 3.  
 DR SMART; SW00409; IgC1; 3.  
 DR SMART; SW00406; Ig; 1.  
 DR PROSITE; PS50035; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.

SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 97.6%; Score 1722; DB 2; Length 466;  
 Best Local Similarity 97.3%; Pred. No. 1.5e-117; Mismatches 5; Indels 0; Gaps 0;  
 Matches 321; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKCPSPVFLAPSSRKSSTGSGTAAGCLVQDYPPPTVWNSGALTSGHATPPAVLQSS 60  
 Db 137 ASTKCPSPVFLAPSSRKSSTGSGTAAGCLVQDYPPPTVWNSGALTSGHATPPAVLQSS 195  
 QY 61 GLYSISSLSSVTVTPSSSLGGTGTGTYICNNHKPENTKVKVKVVEKSKSCKHTCPCPAPELLGG 120  
 Db 197 GLYSISSLSSVTVTPSSSLGGTGTGTYICNNHKPENTKVKVKVVEKSKSCKHTCPCPAPELLGG 256  
 QY 121 PSVFLFPPKKDTLMISRPTVTCTVWDVSHEDPEVKENMYDGEVHNWTKPREEQYN 180  
 Db 257 PSVFLFPPKKDTLMISRPTVTCTVWDVSHEDPEVKENMYDGEVHNWAKTKPREEQYN 316  
 QY 181 STYRVSVLTVLHQWLNGKEYKCKISNKAQPAPEKTIKAKVPRFQVYTLPPSRDE 240  
 Db 317 STYRVSVLTVLHQWLNGKEYKCKISNKAQPAPEKTIKAKVPRFQVYTLPPSRDE 375  
 QY 241 LTKNOVSLTCLVKQFYPSDIAVEWESNGOPENNYKTPPVLDVSQSPFLYSKLTVDKSRW 300  
 Db 377 LTKNOVSLTCLVKQFYPSDIAVEWESNGOPENNYKTPPVLDVSQSPFLYSKLTVDKSRW 436  
 QY 301 QQGNVFSCSYMEHALHNHYQQRSLSLSPGK 330  
 Db 437 QQGNVFSCSYMEHALHNHYQQRSLSLSPGK 466



CC	hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis; severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-1 diabetes mellitus or multiple sclerosis, and for preventing off, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgG1 heavy chain constant region
SQ	Sequence 330 AA;
	Query Match 100%; Score 1754; DB 6; Length 330;
	Best Local Similarity 100.0%; Pred. No. 4e-125;
	Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 ASTKGDSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNAGALTSGVHTFPALQSS 60
	1 ASTKGDSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNAGALTSGVHTFPALQSS 60
QY	61 GLYSISSLSSVVTVPSSIGTQTYICNHNKPSPNTKVKRVEKSCDKHTCPCPAELGG 120
	61 GLYSISSLSSVVTVPSSIGTQTYICNHNKPSPNTKVKRVEKSCDKHTCPCPAELGG 120
Db	121 PSVFLFPKPDKTMISRTPEVTCVWDVSHEDPEPKFNWVUDGVEVHNTKTPREQYN 180
	121 PSVFLFPKPDKTMISRTPEVTCVWDVSHEDPEPKFNWVUDGVEVHNTKTPREQYN 180
QY	181 STYRVSVLTVLHQPNNGKEYKCKVSKNKLPAPEKTIKAKVOPREPOVYTSPSRDE 240
	181 STYRVSVLTVLHQPNNGKEYKCKVSKNKLPAPEKTIKAKVOPREPOVYTSPSRDE 240
Db	241 LTKNOVSLTCLVKGPYPSDIAVEWENQOPENNYKTPPVDSSPEPFYLSKLTWDSRW 300
	241 LTKNOVSLTCLVKGPYPSDIAVEWENQOPENNYKTPPVDSSPEPFYLSKLTWDSRW 300
QY	301 QGNVFSCSVHEALHNHYQRSLSISPGK 330
	301 QGNVFSCSVHEALHNHYQRSLSISPGK 330
Db	3.01 QGNVFSCSVHEALHNHYQRSLSISPGK 330
	3.01 QGNVFSCSVHEALHNHYQRSLSISPGK 330
RESULT 2	
AAB04071	
ID AAB04071 standard; protein; 330 AA.	
XX	
AC AAB04071;	
XX	
DT 11-APR-2001 (first entry)	
DB Zcytor 10:IGG gamma fusion peptide.	
XX	
XX	zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand; binding; detection; modulation; recombinant cell; haematopoietic cell; lymphoid cell; myeloid cell; lymph; immune system; blood; bone; inflammatory response; inflammation; spleen; human.
XX	
OS Synthetic.	
OS Homo sapiens.	
XX	
PN WO200068381-A1.	
XX	
PD 16 - NOV-2000.	
XX	
PP 11-MAY-2000; 2000WO-US012924.	
PR 11-MAY-1999; 99US-00309861.	
XX	
PA (ZYMO ) ZYMOGENETICS INC.	
XX	
PT Presnell SR, Foster DC, Hammond NK, Lok S;	
XX	
DR WPI; 2001-016096/02.	
DR N-PSDB; AAS54473.	
XX	
New cytokine receptor mouse zcytor 10, useful for detecting ligands that	

PT stimulate proliferation or development of hematopoietic, lymphoid and  
 XX myeloid cells.  
 PS Example 17; Page 120-121; 134pp; English.  
 XX  
 CC Isolating a nucleotide which encodes the zcytor 10 cytokine receptor  
 CC enables the production of recombinant cells expressing the receptor.  
 CC Those cells can then be used to detect the presence of a modulator of  
 CC zcytor10 protein by culturing the cells in the presence of a test ligand  
 CC and comparing levels of activity of mouse zcytor10 in the presence and  
 CC absence of the test sample. Similarly, detection of zcytor10 receptor  
 CC ligand within a test sample can be achieved. The method comprising  
 CC contacting a test sample containing an amino acid sequence from Cys15 or  
 CC Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the  
 CC binding of the polypeptide to a ligand in the sample. Specified peptide  
 CC fragments of the zcytor 10 cytokine receptor and the methods described  
 CC are used to identify ligands that stimulate the proliferation and/or  
 CC development of haematopoietic, lymphoid and myeloid cells. Peptide  
 CC fragments of the cytokine receptor are useful for treating lymphoid,  
 CC immune, inflammatory, aplastic, blood or bone disorders and for generating  
 CC antibodies directed against the receptor. A vector expressing a secreted  
 CC human zcytor 10 heterodimer is constructed. In this construct the heavy  
 CC chain of IgG gamma and the extracellular portion of the the heteromeric  
 CC cytokine receptor subunit (an interleukin receptor subunit) is fused to  
 CC human kappa light chain (See GENSEQ record AAA5474). The two sequences  
 CC are fused together using two primers (ACA5475, AAA5476)  
 XX SQ Sequence 330 AA:  
 Query Match 98.0%; Score 1729; DB 4; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122; Indels 0; Gaps 0;  
 Matches 323; Conservative 3; Mismatches 0;  
 QY 1 ASTKGGSVFPALPSSSSTSGGTAALGCLVKDQYFPEPDVTSMNSGALTSGVHTPAVLQSS 60  
 Db 1 ASTKGGSVFPALPSSSSTSGGTAALGCLVKDQYFPEPDVTSMNSGALTSGVHTPAVLQSS 60  
 QY 61 GLYSLSSVWTVTPSSSLGTQTYCINVNHKPSNTKVDKRVEPKSCDKHTCPCCPAPBLGG 120  
 Db 61 GLYSLSSVWTVTPSSSLGTQTYCINVNHKPSNTKVDKRVEPKSCDKHTCPCCPAPBLGG 120  
 QY 121 PSVFLPPKPKDTIMSRTPETCVVVDVSDPEVKFNWYDGVHVNWKTPREQYN 180  
 Db 121 PSVFLPPKPKDTIMSRTPETCVVVDVSDPEVKFNWYDGVHVNWKTPREQYN 180  
 QY 181 STYRVSVLTVLHQNNWNGKEYKCKTISKNSKALPAPETKTISAKVQVRPQQVTLPPSRDE 240  
 Db 181 STYRVSVLTVLHQNNWNGKEYKCKTISKNSKALPAPETKTISAKVQVRPQQVTLPPSRDE 240  
 QY 241 LTRKNQSLTCLVKGFPYPSDIAVEWESNGOPENNYKTPPVLDVSGSPRLPLYSKLTVDKSRW 300  
 Db 241 LTRKNQSLTCLVKGFPYPSDIAVEWESNGOPENNYKTPPVLDVSGSPRLPLYSKLTVDKSRW 300  
 QY 301 QGQNVSCSVMHEALHNHYQQRSLISPGK 330  
 Db 301 QGQNVSCSVMHEALHNHYQQRSLISPGK 330

RESULT 3  
 IDAAM4756  
 XX AAAM47856 standard; protein; 330 AA.  
 AC  
 XX  
 XX  
 DT 22-FEB-2002 (first entry)  
 DE Human Ig-gamma1 heavy chain constant region amino acid sequence.  
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
 KW transgenic plant.  
 XX





KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.  
 XX Homo sapiens.

OS WO200200721-A2.

PN XX ID ABP71856 standard; protein; 330 AA.

PD XX AC ABP71856;

XX PR 26-JUN-2001; 2001WO-US020484.

PR 26-JUN-2000; 2000US-0214282P.

PR 29-JUN-0000; 2000US-0214955P.

PR 08-FEB-2001; 2001US-0267963P.

XX PA (ZYMO ) ZYMOGENETICS INC.

PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;

PI Maurer MF;

XX DR WPI; 2002-090519/12.

DR N-PSDB; ABA93797.

XX PT Isolated polynucleotide encoding a cytokine receptor designated zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.

PT XX PS Example 17; Page 187-188; 235PP; English.

CC The present invention describes a cytokine receptor designated zcytor17. zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, anti-rheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABA95730 to ABB05745 represent sequences used in the exemplification of the present invention

XX SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330; Best Local Similarity 97.9%; Pred. No. 1.8e-122; Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

CC QY 1 ASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPERPVTVSNRSGALTSGVHIFTPAVLQSS 60

CC 1 ASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPERPVTVSNRSGALTSGVHIFTPAVLQSS 60

CC 61 GLYSLSVVTPSSGLGTQTYICNVNPKSNTKVDKVKPEPKSCDKHTCPCPAPBLIGG 120

CC 61 GLYSLSVVTPSSGLGTQTYICNVNPKSNTKVDKVKPEPKSCDKHTCPCPAPBLIGG 120

CC 121 PSVLFLEPPKKPDKTLMISRTPETVTVWDVSHDPEVKENWYTDGVENVHVKTPREQYN 180

CC 121 PSVLFLEPPKKPDKTLMISRTPETVTVWDVSHDPEVKENWYTDGVENVHVKTPREQYN 180

CC 181 STRRVVSVLTVLHQDWLNGKEYKCKVSKNKA  
Db 181 STRRVVSVLTVLHQDWLNGKEYKCKVSKNKA  
Db 181 STRRVVSVLTVLHQDWLNGKEYKCKVSKNKA  
Db 241 LTKNQVSLTCLYKGFYSDIAWEWSNGOPENNYKTTPVLDGSPFLYSLKTVKSRW 300

Db 241 LTKNQVSLTCLYKGFYSDIAWEWSNGOPENNYKTTPVLDGSPFLYSLKTVKSRW 300

CC QY 61 GLYSLSVVTPSSGLGTQTYICNVNPKSNTKVDKVKPEPKSCDKHTCPCPAPBLIGG 120

CC QY 61 GLYSLSVVTPSSGLGTQTYICNVNPKSNTKVDKVKPEPKSCDKHTCPCPAPBLIGG 120

XX SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330; Best Local Similarity 97.9%; Pred. No. 1.8e-122; Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

CC QY 1 ASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPERPVTVSNRSGALTSGVHIFTPAVLQSS 60

CC 1 ASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPERPVTVSNRSGALTSGVHIFTPAVLQSS 60

Db 61 GLYSLSVVTVPPSSIGTGTICNWKPSNTKVDKVKVPEKSCKTHCPCPAPELGG 120  
 QY 121 PSVFLPPKKDTLMISRTEVTCTVWVDSHEDPEVKFNYDGVVEHNVTKRREQVN 180  
 Db 121 PSVFLPPKKDTLMISRTEVTCTVWVDSHEDPEVKFNYDGVVEHNVTKRREQVN 180  
 QY 181 STYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPVYTLLPSRDE 240  
 Db 181 STYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPVYTLLPSRDE 240  
 QY 241 LTKNOVSLCLVKGVPSPDAVEWSNGOPENNYKTPVLDGSFFEYSLKLTVDKRW 300  
 Db 241 LTKNOVSLCLVKGVPSPDAVEWSNGOPENNYKTPVLDGSFFEYSLKLTVDKRW 300  
 QY 301 QQGNVFSCSVMHEALHNHYQKSLSLSPK 330  
 Db 301 QQGNVFSCSVMHEALHNHYQKSLSLSPK 330

**RESULT 8**

AAE32915 standard; protein; 330 AA.  
 ID AAE32915 standard; protein; 330 AA.  
 AC AAE32915;  
 XX DT 24-MAR-2003 (first entry)  
 DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.  
 XX KW T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.  
 OS Homo sapiens.  
 XX PN WO200279232-A2.  
 PD 10-OCT-2002.  
 XX PR 30-MAR-2002; 2002WO-US009815.  
 XX PR 30-MAR-2001; 2001US-0280625P.  
 PA (LEXI-) LEXIGEN PHARM CORP.  
 XX PI Gillies SD;  
 DR XX  
 PT WPI; 2003-103259/09.

Reducing the immunogenicity of a fusion protein comprises changing an amino acid within the Junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to interact with T-cell receptor.

**Disclosure:** Page 49-50; 68pp; English.

The invention relates to a method for reducing the immunogenicity of a fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the Junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analyzing, changing or modifying one or more amino acids in the Junction region of a fusion protein to identify a T-cell epitope and within a junction spanning a fusion junction of a fusion protein. The less immunogenic fusion proteins are useful in providing therapeutic treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region used to illustrate the method of the invention Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122; Matches 323; Conservative 3; Mismatches 4; Idents 0; Gaps 0; Gaps 0;

Db 61 GLYSLSVVTVPPSSIGTGTICNWKPSNTKVDKVKVPEKSCKTHCPCPAPELGG 120  
 QY 1 ASTKGPSVFLPARKSSKSTSGTAALGCLVYDFPFPVTVNSNALTSGWHTPAVLOSS 60  
 Db 1 ASTKGPSVFLPARKSSKSTSGTAALGCLVYDFPFPVTVNSNALTSGWHTPAVLOSS 60  
 QY 61 GLYSLSVVTVPPSSIGTGTICNWKPSNTKVDKVKVPEKSCKTHCPCPAPELGG 120  
 Db 121 PSVFLPPKKDTLMISRTEVTCTVWVDSHEDPEVKFNYDGVVEHNVTKRREQVN 180  
 QY 181 STYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPVYTLLPSRDE 240  
 Db 181 STYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPVYTLLPSRDE 240  
 QY 241 LTKNOVSLCLVKGVPSPDAVEWSNGOPENNYKTPVLDGSFFEYSLKLTVDKRW 300  
 Db 241 LTKNOVSLCLVKGVPSPDAVEWSNGOPENNYKTPVLDGSFFEYSLKLTVDKRW 300  
 QY 301 QQGNVFSCSVMHEALHNHYQKSLSLSPK 330  
 Db 301 QQGNVFSCSVMHEALHNHYQKSLSLSPK 330

**RESULT 9**

AAE32627 standard; protein; 330 AA.  
 ID AAE32627 standard; protein; 330 AA.  
 AC AAE32627;  
 XX DT 24-MAR-2003 (first entry)  
 DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.  
 XX KW Human; immunogenic; therapy; immunoglobulin G1; IgG1.  
 OS Homo sapiens.  
 XX PN WO200279415-A2.  
 PD 10-OCT-2002.  
 XX PR 29-MAR-2002; 2002WO-US009650.  
 XX PR 30-MAR-2001; 2001US-0280625P.  
 PA (LEXI-) LEXIGEN PHARM CORP.  
 XX PI Gillies SD;  
 DR XX  
 PT WPI; 2003-111794/10.

Reducing the immunogenicity of a fusion protein by changing an amino acid within the Junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor.

**Disclosure:** Page 49-50; 67pp; English.

Reducing the immunogenicity of a fusion protein by changing an amino acid within the Junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor.

The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the Junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of fusion proteins for use in therapy. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the method of the invention Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122; Matches 323; Conservative 3; Mismatches 4; Idents 0; Gaps 0; Gaps 0;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSSKSTSGTAAGCLVVDYFPPEVTWSNSGALTSGVHTFPALQSS 60  
 Db 1 ASTKGPSVPLAPSSKSTSGTAAGCLVVDYFPPEVTWSNSGALTSGVHTFPALQSS 60  
 Qy 61 GLYSLSVVTVPPSSSLGQTQYICNVMHKPSNTKVDKKVEPKSCDKTHTCPCPABLLGG 120  
 Db 61 GLYSLSVVTVPPSSSLGQTQYICNVMHKPSNTKVDKKVEPKSCDKTHTCPCPABLLGG 120  
 Qy 181 STYRVVSLTILHQWMNGKEYKCKVSKNKLPAPEKTIKAKVQPREPOVYUPLPSDE 240  
 Db 181 STYRVVSLTILHQWMNGKEYKCKVSKNKLPAPEKTIKAKVQPREPOVYUPLPSDE 240  
 Qy 121 PSVLEFPPKDTLMSRTPETCVVWVDSHEDPEVKENNYVTDGVYEVNKTKEPEQYN 180  
 Db 121 PSVLEFPPKDTLMSRTPETCVVWVDSHEDPEVKENNYVTDGVYEVNKTKEPEQYN 180  
 Qy 241 LTKNQSLTCLVKGVGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLPSKLTVDKSRW 300  
 Db 241 LTKNQSLTCLVKGVGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLPSKLTVDKSRW 300  
 Qy 301 QGNVFSCSVNHEALHNHYDORSLSPGK 330  
 Db 301 QGNVFSCSVNHEALHNHYDORSLSPGK 330

RESULT 10

ID ABR82103 standard; protein; 330 AA.  
 AC ABR82103;  
 XX DT 23-SEP-2003 (first entry)  
 DE Human DR6 related amino acid sequence SEQ ID NO:5.  
 KW Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;  
 KW antiarthritic; dermatological; antiinflammatory; thyromimetic;  
 KW hepatotropic; nephrotropic; antidiabetic; antihypertrophic; antifungal;  
 KW antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.  
 XX OS Homo sapiens.  
 XX PN WO2003051290-A2.  
 XX PD 26-JUN-2003.  
 XX PR 10-DEC-2002; 2002WO-US037596.  
 XX PR 17-DBC-2001; 2001US-0342632P.  
 XX PA (ELIL ) LILLY & CO ELL .  
 XX PI Liu J, Na S, Song HY, Yang D;  
 XX DR WPI: 2003-541604/51.

XX PT Treating or preventing a B cell mediated condition e.g., chronic hepatitis or chronic cirrhosis, in a mammal by administering a pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to the mammal.  
 XX Disclosure; Page 96-97; 97pp; English.

XX CC The present invention describes a method (M1) for treating or preventing a B cell mediated condition in a mammal by administering a pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to the mammal, by also described: (1) inhibiting B cell mediated immunity in a mammal, by

CC administering a pharmaceutical composition comprising at least one DR6 agonist; (2) use of a dr6 agonist in the manufacture of a medicament for treating or preventing at least one symptom associated with conditions (C1) such as aberrant apoptosis, graft-versus-host disease (GVHD), atopy, rheumatoid arthritis, asthma, eczema, inflammatory bowel disease, cancer, vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancreatitis, psoriasis, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease, transplant rejection, systemic lupus erythematosus, Behcet's disease, autoimmune nephropathy, autoimmune haematoxathy, idiopathic interstitial pneumonia, hypersensitivity pneumonitis, autoimmune dermatosis, autoimmune cardiopathy, autoimmune infertility, autoimmune gastritis, fibroesing lung disease, fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, Helicobacter pylori-associated ulceration, organ rejection after transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic purpura (TTP) and haemolytic uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MDS), adult respiratory distress syndrome (ARDS), and at least one condition or symptom related to the conditions, in a mammal; and (3) use of DR6 antagonist in the manufacture of a medicament for treating or preventing at least one symptom associated with conditions (C2) such as aberrant apoptosis, immunodeficiency, bacterial infection, viral infection, microbial infection, complications of infection, HIV, HIV-induced lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori-associated ulceration, cytoprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, and at least one condition or symptom related to the conditions, in a mammal. DR6 has immunosuppressive, antidiabetic, anti-HIV, antiasthmatic, dermatological, antiinflammatory, antidiabetic, nephrotropic, antidiabetic, antihypertrophic, antifungal, antiviral, antibacterial, antidiabetic, antihypertrophic, antidiabetic, antimicrobial and anti-HIV activities. (M1) is useful for treating or preventing at least one symptom associated with (C1) in a mammal, preferably human, by administering DR6 agonist, and for treating or preventing at least one symptom associated with (C2) by administering DR6 antagonist. The present sequence represents a human DR6 related amino acid sequence, which is given in the exemplification of the present invention

SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSSKSTSGTAAGCLVVDYFPPEVTWSNSGALTSGVHTFPALQSS 60  
 Db 1 ASTKGPSVPLAPSSKSTSGTAAGCLVVDYFPPEVTWSNSGALTSGVHTFPALQSS 60  
 Qy 61 GLYSLSVVTVPPSSSLGQTQYICNVMHKPSNTKVDKKVEPKSCDKTHTCPCPABLLGG 120  
 Db 61 GLYSLSVVTVPPSSSLGQTQYICNVMHKPSNTKVDKKVEPKSCDKTHTCPCPABLLGG 120  
 Qy 181 STYRVVSLTILHQWMNGKEYKCKVSKNKLPAPEKTIKAKVQPREPOVYUPLPSDE 240  
 Db 181 STYRVVSLTILHQWMNGKEYKCKVSKNKLPAPEKTIKAKVQPREPOVYUPLPSDE 240  
 Qy 121 PSVLEFPPKDTLMSRTPETCVVWVDSHEDPEVKENNYVTDGVYEVNKTKEPEQYN 180  
 Db 121 PSVLEFPPKDTLMSRTPETCVVWVDSHEDPEVKENNYVTDGVYEVNKTKEPEQYN 180  
 Qy 241 LTKNQSLTCLVKGVGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLPSKLTVDKSRW 300  
 Db 241 LTKNQSLTCLVKGVGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLPSKLTVDKSRW 300  
 Qy 301 QGNVFSCSVNHEALHNHYDORSLSPGK 330  
 Db 301 QGNVFSCSVNHEALHNHYDORSLSPGK 330

RESULT 11

AA031102

ID	AAC31102 standard; protein; 330 AA.	XX	XX	XX
AC	AA031102;	AC	ABR55836;	
XX		XX	XX	
DT	06-OCT-2003 (first entry)	DT	02-SEP-2003 (first entry)	
XX		XX	XX	
DE	Human A2-G8 SCF antibody heavy chain constant region.	DE	Anti-Ang-2 antibody IgG1 constant region.	
XX		XX	XX	
KW	Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;	KW	Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;	
KW	steel factor; c-kit ligand; gene therapy; heavy chain.	KW	gynaecological; antiinflammatory; osteopathic; antiporiatic; cancer;	
XX		KW	angiogenesis; antibody; human.	
OS	Homo sapiens.	OS	Homo sapiens.	
XX		XX	XX	
PN	WO2003051311-A2.	PN	WO2003030833-A2.	
XX		XX	XX	
PD	26-JUN-2003.	PD	17-APR-2003.	
XX		XX	XX	
PP	16-DEC-2002; 2002WO-US040227.	PP	11-OCT-2002; 2002WO-US032613.	
XX		XX	XX	
PR	17-DBC-2001; 2001US-0342174P.	PR	11-OCT-2001; 2001US-0328604P.	
XX		PR	10-OCT-2002; 2002US-00269805.	
PA	(FARB ) BAYER CORP.	PA	(AMGB-) AMGEN INC.	
XX		XX	XX	
PI	Takeuchi T, Tomkinson A, Neben S;	PI	Oliner JD;	
XX		XX	XX	
DR	WPI; 2003-523500/49.	DR	WPI; 2003-504963/47.	
XX		XX	XX	
N-PSDB; AAL62618.				
PS	New purified human antibody that binds to stem cell factor protein, useful for preparing a composition for treating asthma.	PT	New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.	
XX		PT	PT	
CC	The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain constant region	CC	The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disorders, atherosclerosis, endometriosis, neoplastic disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a human IgG1 constant region of an anti-Ang-2 antibody	
CC		CC	CC	
XX		CC	CC	
PS	Example 10; Page 47-48; 94pp; English.	PS	Example 4; Page 96; 161pp; English.	
XX		XX	XX	
CC	Best Local Similarity 97.9%; Pred. No. 1.8e-122; Indels 0; Gaps 0; Matches 323; Conservative 3; Mismatches 4; Insertions 0; Deletions 0; Sequence 330 AA;	CC	Best Local Similarity 97.9%; Pred. No. 1.8e-122; Indels 0; Gaps 0; Matches 323; Conservative 3; Mismatches 4; Insertions 0; Deletions 0; Sequence 330 AA;	
CC		CC	CC	
Db	1 ASTKGPSVFLAPSKSTGGTALGCLVKDLYFPEVTVSNAGALTSGHHTPAVLQSS 60	Db	1 ASTKGPSVFLAPSKSTGGTALGCLVKDLYFPEVTVSNAGALTSGHHTPAVLQSS 60	
Db	1 ASTKGPSVFLAPSKSTGGTALGCLVKDLYFPEVTVSNAGALTSGHHTPAVLQSS 60	Db	1 ASTKGPSVFLAPSKSTGGTALGCLVKDLYFPEVTVSNAGALTSGHHTPAVLQSS 60	
Qy	61 GLYLSLSSVVTVPSSSLGTOTIVCNVNHKPSNTKVDKRVKEPKSCDKHTCPCPAPBLLGG 120	Qy	61 GLYLSLSSVVTVPSSSLGTOTIVCNVNHKPSNTKVDKRVKEPKSCDKHTCPCPAPBLLGG 120	
Db	61 GLYLSLSSVVTVPSSSLGTOTIVCNVNHKPSNTKVDKRVKEPKSCDKHTCPCPAPBLLGG 120	Db	61 GLYLSLSSVVTVPSSSLGTOTIVCNVNHKPSNTKVDKRVKEPKSCDKHTCPCPAPBLLGG 120	
Qy	121 PSVFLFPKKDKDTIMSRTPETVTCVVDVSHEDPEVKENWVVDGEVHNWYKTKPREGQVN 180	Qy	121 PSVFLFPKKDKDTIMSRTPETVTCVVDVSHEDPEVKENWVVDGEVHNWYKTKPREGQVN 180	
Db	121 PSVFLFPKKDKDTIMSRTPETVTCVVDVSHEDPEVKENWVVDGEVHNWYKTKPREGQVN 180	Db	121 PSVFLFPKKDKDTIMSRTPETVTCVVDVSHEDPEVKENWVVDGEVHNWYKTKPREGQVN 180	
Qy	181 STYRVISVLTILHQMLNGKEYKCKVSKNKLPAPEKTIKAKVQPREQVYTLPPSRDE 240	Qy	181 STYRVISVLTILHQMLNGKEYKCKVSKNKLPAPEKTIKAKVQPREQVYTLPPSRDE 240	
Db	181 STYRVISVLTILHQMLNGKEYKCKVSKNKLPAPEKTIKAKVQPREQVYTLPPSRDE 240	Db	181 STYRVISVLTILHQMLNGKEYKCKVSKNKLPAPEKTIKAKVQPREQVYTLPPSRDE 240	
Qy	241 LTKNOVSLTICLVKGTFPSDIAVEWESNGOPENNYKTPPVLDGSFFPLSKLTVDSKRW 300	Qy	241 LTKNOVSLTICLVKGTFPSDIAVEWESNGOPENNYKTPPVLDGSFFPLSKLTVDSKRW 300	
Db	241 LTKNOVSLTICLVKGTFPSDIAVEWESNGOPENNYKTPPVLDGSFFPLSKLTVDSKRW 300	Db	241 LTKNOVSLTICLVKGTFPSDIAVEWESNGOPENNYKTPPVLDGSFFPLSKLTVDSKRW 300	
Qy	301 QQGNVFSCSVMHEALHNHYTOKSLSPGK 330	Qy	301 QQGNVFSCSVMHEALHNHYTOKSLSPGK 330	
Db	301 QQGNVFSCSVMHEALHNHYTOKSLSPGK 330	Db	301 QQGNVFSCSVMHEALHNHYTOKSLSPGK 330	
RESULT 12				
ABR55835				
ABR55836	standard; protein; 330 AA.			

RESULT 13  
 Qy 301 QQGNVFSCSVHEALHNHYQORSLSLSPGK 330  
 Db 301 QQGNVFSCSVHEALHNHYQORSLSLSPGK 330

AA030893  
 ID AAO30893 standard; protein; 330 AA.  
 AC ADF11389;  
 XX  
 XX Human immunoglobulin gamma (IgG) 1 constant region.

XX  
 DE Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;  
 KW gene therapy; immunoglobulin; Ig; human.  
 XX  
 OS Homo sapiens.  
 OS XX  
 PN WO2003048334-A2.  
 PR 12-JUN-2003.  
 XX  
 PF 04-DEC-2002; 2002WO-US038780.  
 PN XX  
 PR 04-DEC-2001; 2001US-0337113P.  
 PR 12-APR-2002; 2002US-0371966P.  
 XX  
 PA (EMBL-) EMD LEXIGEN RES CENT CORP.  
 PR XX  
 PT Gillies SD;  
 PI DR  
 XX  
 PS New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2  
 PT moiety, useful for preparing a composition for treating cancer, viral  
 PT infections or immune disorders.  
 XX  
 Example 1; Page 51-53; 71pp; English.

XX  
 CC The invention relates to cytokine fusion proteins with increased  
 CC therapeutic index and methods for increasing the therapeutic index of  
 such fusion proteins. The fusion protein comprises a non-interleukin-2  
 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a  
 CC composition for treating cancer, viral infections or immune disorders.  
 CC The fusion protein is also used in gene therapy. The present sequence is  
 CC used in gene therapy. The present sequence is used  
 CC to illustrate the method of the invention  
 XX  
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAALGCLVDYFPERPVTSWNAGLTSGVHTFPVLOSS 60  
 Db 1 ASTKGPSVFLAPSSKSTSGTAALGCLVDYFPERPVTSWNAGLTSGVHTFPVLOSS 60

61 GLYSLSSWVTPSSLGTQTYICVNHHKPNTKVKVKEPKSCDKHTCPCPAPLLGG 120  
 61 GLYSLSSWVTPSSLGTQTYICVNHHKPNTKVKVKEPKSCDKHTCPCPAPLLGG 120

121 PSVFLPPKPDLMISRPTPTCWVWDVSHEDPEVFKENWVDDGVFVHNRTKPRREQYN 180  
 121 PSVFLPPKPDLMISRPTPTCWVWDVSHEDPEVFKENWVDDGVFVHNRTKPRREQYN 180

181 STYRVVSLVTLHQNMNGKEYKCKVSKNPKLPAPEKTIKAKVPRPEPVYTLPSRDE 240  
 181 STYRVVSLVTLHQDLNGKEYKCKVSKNPKLPAPEKTIKAKVPRPEPVYTLPSRDE 240

Qy 301 QQGNVFSCSVHEALHNHYQORSLSLSPGK 330  
 Db 301 QQGNVFSCSVHEALHNHYQORSLSLSPGK 330

RESULT 14  
 Qy 241 LTKNQVSLTCLVKGRFSPDAVEWSNGQQENNYKUTPPFLDSVSEFLISKLTVDSRW 300  
 Db 241 LTKNQVSLTCLVKGRFSPDAVEWSNGQQENNYKUTPPFLDSVSEFLISKLTVDSRW 300

ADP11389  
 ID ADF11389 standard; protein; 330 AA.  
 AC ADF11389;  
 XX  
 XX Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.  
 XX  
 DE human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;  
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003086289-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 07-APR-2003; 2003WO-US010749.  
 XX  
 PR WO2003086289-A2.  
 XX  
 PR 05-APR-2002; 2002US-0370407P.  
 XX  
 PA (AMG8-) AMGEN INC.  
 PR XX  
 PT Boyle WJ, Medlock B, Sullivan JK, Elliott RL, Martin F, Huang H;  
 XX  
 PT DR N-PSDB; ADF11388.  
 XX  
 PT New isolated antibody that specifically binds osteoprotegerin ligand,  
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,  
 XX bone loss from arthritis, Paget's disease or osteopenia.  
 PS Example 3; SEQ ID NO 2; 156pp; English.

XX  
 CC The present invention describes an isolated human antibody (1) that  
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
 pharmaceutical composition comprising a pharmaceutical carrier and a  
 therapeutic amount of (1); (2) methods of treating an osteopenic disorder  
 CC in a patient, comprising administering to a patient the pharmaceutical  
 composition of (1) or a pharmaceutical amount of (1); and (3) a method  
 CC for detecting OPGL in a biological sample, comprising contacting the  
 sample with (1) under conditions that allow for binding of the antibody  
 CC to OPGL, and measuring the level of bound antibody in the sample. (1) has  
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in  
 gene therapy. The composition and methods are useful in diagnosing or  
 treating bone disorders, such as osteoporosis, bone loss from arthritis,  
 CC Paget's disease or osteopenia. The antibody (1) may also be used for  
 detecting OPGL in biological samples and in identifying cells or tissues  
 CC that produce the protein. The present sequence represents a sequence  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 7; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAALGCLVDYFPERPVTSWNAGLTSGVHTFPVLOSS 60  
 Db 1 ASTKGPSVFLAPSSKSTSGTAALGCLVDYFPERPVTSWNAGLTSGVHTFPVLOSS 60

QY	61 GLYSASSVVVPSSGLGTGTYICNNHKCSNTKVKVVEKSCKTHTCPGPCPAPELGG 120	XX	
Db	61 GLYSASSVVVPSSGLGTGTYICNNHKCSNTKVKVVEKSCKTHTCPGPCPAPELGG 120	SQ	Sequence 330 AA;
Qy	121 PSVFLPPKKDKTMSRTPEVTCVWDVSHEDEPVENWYDGVEVHVKTKREEQN 180	Query Match	98.0%; Score 1729; DB 7; Length 330;
Db	121 PSVFLPPKKDKTMSRTPEVTCVWDVSHEDEPVENWYDGVEVHVKTKREEQN 180	Best Local Similarity	97.9%; Pred. No. 1.8e-122;
Qy	181 STYRVNSVLTVLHQDWLNGKEYKCKVSKNKLPAPEKTISAKVOPREPOVYTLPSSRDE 240	Matches	323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Db	181 STYRVNSVLTVLHQDWLNGKEYKCKVSKNKLPAPEKTISAKVOPREPOVYTLPSSRDE 240	Qy	1 ASTKAPSVPFLAPSSKSTSGTAALGCLVYDFEPBVVWSNAGALTSGVHTEPAVLOSS 60
Qy	241 LTQNQSLTCLVKGKGPDSIAVENEWSNGQPENNYKTPPLDSGSFFLYSKLTVDKSRW 300	Db	1 ASTKGPSVPFLAPSSKSTSGTAALGCLVYDFEPBVVWSNAGALTSGVHTFPAVLOSS 60
Db	241 LTQNQSLTCLVKGKGPDSIAVENEWSNGQPENNYKTPPLDSGSFFLYSKLTVDKSRW 300	Qy	61 GLYSASSVVVPSSGLGTGTYICNNHKCSNTKVKVVEKSCKTHTCPGPCPAPELGG 120
Qy	301 QQGNVFSCSTMHEALHNHQRSLSLSPKG 330	Db	61 GLYSASSVVVPSSGLGTGTYICNNHKCSNTKVKVVEKSCKTHTCPGPCPAPELGG 120
Db	301 QQGNVFSCSTMHEALHNHQRSLSLSPKG 330	Qy	121 PSVFLPPKKDKTMSRTPEVTCVWDVSHEDEPVENWYDGVEVHVKTKREEQN 180
RESULT	15	Db	121 PSVFLPPKKDKTMSRTPEVTCVWDVSHEDEPVENWYDGVEVHVKTKREEQN 180
ID	AD97351 standard; protein; 330 AA.	Qy	181 STYRVNSVLTVLHQDWLNGKEYKCKVSKNKLPAPEKTISAKVOPREPOVYTLPSSRDE 240
AC	AD97351;	Db	181 STYRVNSVLTVLHQDWLNGKEYKCKVSKNKLPAPEKTISAKVOPREPOVYTLPSSRDE 240
XX	12-FEB-2004 (first entry)	Qy	241 LTQNQSLTCLVKGKGPDSIAVENEWSNGQPENNYKTPPLDSGSFFLYSKLTVDKSRW 300
XX	Human IgG1 heavy chain constant region protein - SEQ ID 20.	Db	241 LTQNQSLTCLVKGKGPDSIAVENEWSNGQPENNYKTPPLDSGSFFLYSKLTVDKSRW 300
KW	immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin; virucide; antibacterial; anthrax; rhinovirus infection; common cold; intercellular adhesion molecule; ICAM-1; human; constant region; IgG.	Qy	301 QQGNVFSCSTMHEALHNHQRSLSLSPKG 330
XX	Homo sapiens.	Db	301 QQGNVFSCSTMHEALHNHQRSLSLSPKG 330
XX	WO2003064992-A2.	Search completed: June 7, 2005, 08:56:37	
PN		Job time : 172.565 secs	
XX	07-AUG-2003.		
PD			
PF	25-OCT-2002; 2002WO-US034197.		
PR	26-OCT-2001; 2001US-00047542.		
XX	(PLAN-) PLANET BIOTECHNOLOGY INC.		
PA	(LARR-) LARRICK J W.		
PA	(WYCO/) WYCOFF K L.		
XX	Larrick JW, Wycoff KL;		
PI	XX		
PT	WPI; 2003-636816/60.		
DR	N-RSDB; ADE97350, ADE97376.		
XX	New immunoadhesin, useful for treating anthrax and rhinovirus, comprises chimeric toxin receptor protein linked to immunoglobulin heavy chain, and J chain and secretory component associated with the chimeric toxin receptor protein.		
XX	Disclosure; SEQ ID NO 20; 288pp; English.		
CC	The invention relates to a novel immunoadhesin comprising a chimeric toxin receptor protein consisting of a toxin receptor protein linked to at least a portion of an immunoglobulin heavy chain with a J (joining) chain and secretory component (SC) associated with the chimeric toxin receptor protein. The immunoadhesin comprises a chimeric bacterial or viral toxin receptor protein and the immunoadhesin has plant-specific glycosylation. The immunoadhesin of the invention demonstrates virucide and antibacterial activities and may be useful for reducing the binding of a viral or bacterial antigen to a host cell and thus for treating or preventing anthrax, as well as human rhinovirus infection which results in the common cold. The current sequence is that of the human immunoadhesion-related protein of the invention.		

Run on: June 7, 2005, 09:01:44 ; Search time 144.767 Seconds  
           (w/o alignments)  
           821.093 Million cell updates/sec

Title: Perfect score: US-11-000-439-2

Sequence: 1 ASTKGPSVFLPAPSSKSTSG.....MHEALHNWYQQRSLSLSPK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1595520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 159520

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
           Maximum Match 100%  
           Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/podata/1/pupbaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/podata/1/pupbaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/podata/1/pupbaa/US06\_PUBCOMB.pep:\*

4: /cgn2\_6/podata/1/pupbaa/US07\_NEW\_PUB.pep:\*

5: /cgn2\_6/podata/1/pupbaa/PCTUS\_PUBCOMB.pep:\*

6: /cgn2\_6/podata/1/pupbaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/podata/1/pupbaa/US08\_PUBCOMB.pep:\*

8: /cgn2\_6/podata/1/pupbaa/US09A\_PUBCOMB.pep:\*

9: /cgn2\_6/podata/1/pupbaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/podata/1/pupbaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/podata/1/pupbaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/podata/1/pupbaa/US09\_NEW\_PUB.pep:\*

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14: /cgn2\_6/podata/1/pupbaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/podata/1/pupbaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/podata/1/pupbaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/podata/1/pupbaa/US10E\_PUBCOMB.pep:\*

18: /cgn2\_6/podata/1/pupbaa/US11A\_PUBCOMB.pep:\*

19: /cgn2\_6/podata/1/pupbaa/US11\_NEW\_PUB.pep:\*

20: /cgn2\_6/podata/1/pupbaa/US60\_NEW\_PUB.pep:\*

21: /cgn2\_6/podata/1/pupbaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1764	100.0	330	10	US-09-947-208-2
2	1764	100.0	330	14	US-10-000-439-2
3	1729	98.0	330	10	US-09-995-828A-15
4	1729	98.0	330	10	US-09-892-949-38
5	1729	98.0	330	13	US-10-047-545-20
6	1729	98.0	330	14	US-10-269-805-68
7	1729	98.0	330	14	US-10-310-719-8
8	1729	98.0	330	14	US-10-112-582-1
9	1729	98.0	330	14	US-10-320-231A-81
10	1729	98.0	330	15	US-09-383-912A-6
11	1729	98.0	330	15	US-10-080-901-2
12	1729	98.0	330	15	US-10-420-034A-15

RESULTS

US-09-847-208-2

; Sequence 2, Application US/09847208

; Publication No. US20030082190A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; APPLICANT: Zhang, Ke

; APPLICANT: Zhu, Daocheng

; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF FILE REFERENCE: UC67\_002A

; CURRENT APPLICATION NUMBER: US/09/847,208

; CURRENT FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2

; LENGTH: 330

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-847-208-2

Query Match Score 100.0%; Score 1764; DB 10; Length 330; Best Local Similarity 100.0%; Pred. No. 1.1e-128; Mismatches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 330; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKSTSGTAALGCLVKQLYFPEPPTVSNSGALTSGVHTPAVQSS 60

Db 1 ASTKGPSVFLPAPSSKSTSGTAALGCLVKQLYFPEPPTVSNSGALTSGVHTPAVQSS 60

Qy 61 GLYSLSLSSWVTTPSSGLQTOTIICVNWKPSNPKVDKVKEPSCDKHICPPAPELGG 120

Db 61 GLYSLSLSSWVTTPSSGLQTOTIICVNWKPSNPKVDKVKEPSCDKHICPPAPELGG 120

Qy 121 PSVFLPPKPDMLMSRTPSYTCVWDVSDPVEKFKNWYDGVEHANKTKPREEQYN 180

RESULT 2  
US-10-000-439-2  
; Sequence 2, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; FILE REFERENCE: UC067\_004A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIORITY FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-000-439-2

Query Match 98.0%; Score 1729; DB 10; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126; Mismatches 323; Conservative 3; Indels 0; Gaps 0;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVVDYFPERPVWSWNNSGALTSGVHTFPALLOSS 60  
Db 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVVDYFPERPVWSWNNSGALTSGVHTFPALLOSS 60  
Qy 61 GLYSLSSSVVTPSSSLGQTQYICWNNHKPSNTKDKKKVKEPKSCDKHTCPCPABELGG 120  
Db 61 GLYSLSSSVVTPSSSLGQTQYICWNNHKPSNTKDKKKVKEPKSCDKHTCPCPABELGG 120  
Qy 121 PSVFLPPKDKTMSRTPETCVVWDVSHEDEPVKFWYDGVIEVANVKTKREBQN 180  
Db 121 PSVFLPPKDKTMSRTPETCVVWDVSHEDEPVKFWYDGVIEVANVKTKREBQN 180  
Qy 181 STYRVVSLTVLHQMNNGKEYKCKVSNKALPAPIEKTISAKVOPREPOVYTLPSRDE 240  
Db 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVVDYFPERPVWSWNNSGALTSGVHTFPALLOSS 60  
Qy 61 GLYSLSSSVVTPSSSLGQTQYICWNNHKPSNTKDKKKVKEPKSCDKHTCPCPABELGG 120  
Db 61 GLYSLSSSVVTPSSSLGQTQYICWNNHKPSNTKDKKKVKEPKSCDKHTCPCPABELGG 120  
Qy 121 PSVFLPPKDKTMSRTPETCVVWDVSHEDEPVKFWYDGVIEVANVKTKREBQN 180  
Db 121 PSVFLPPKDKTMSRTPETCVVWDVSHEDEPVKFWYDGVIEVANVKTKREBQN 180  
Qy 181 STYRVVSLTVLHQMNNGKEYKCKVSNKALPAPIEKTISAKVOPREPOVYTLPSRDE 240  
Db 181 STYRVVSLTVLHQMNNGKEYKCKVSNKALPAPIEKTISAKVOPREPOVYTLPSRDE 240  
Qy 241 LTKNQVSLTCLVKGYFPSDIAVEMESNGOPENNYKTPPVLDVGSSFFLXSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGYFPSDIAVEMESNGOPENNYKTPPVLDVGSSFFLXSKLTVDKSRW 300  
Qy 301 QQGNVFSCSVNHEALTHYQKSLSLSPGK 330  
Db 301 QQGNVFSCSVNHEALTHYQKSLSLSPGK 330

RESULT 3  
US 09-995-898A-15  
; Sequence 15, Application US/09995898A  
; Publication No. US20030027253A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: NO. US20030027253A1ak, Julia E.

RESULT 4  
US-09-892-949-3B  
; Sequence 38, Application US/0982949  
; Publication No. US20030098339A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Kuijper, Joseph L.  
; APPLICANT: Maurer, Mark F.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
; FILE REFERENCE: 00-422  
; CURRENT APPLICATION NUMBER: US 09/892,949  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,955  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/267,963  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3B  
; LENGTH: 330  
; TYPE: PRT

APPLICANT: Whitmore, Theodore E.  
APPLICANT: Grant, Francis J.  
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
FILE REFERENCE: 00-108  
CURRENT APPLICATION NUMBER: US 09/995,898A  
CURRENT FILING DATE: 2001-11-28  
PRIOR APPLICATION NUMBER: US 60/253,561  
PRIOR APPLICATION NUMBER: US 60/267,211  
PRIOR FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-895-898A-15

Query Match 98.0%; Score 1729; DB 10; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126; Mismatches 323; Conservative 3; Indels 0; Gaps 0;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVVDYFPERPVWSWNNSGALTSGVHTFPALLOSS 60  
Db 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVVDYFPERPVWSWNNSGALTSGVHTFPALLOSS 60  
Qy 61 GLYSLSSSVVTPSSSLGQTQYICWNNHKPSNTKDKKKVKEPKSCDKHTCPCPABELGG 120  
Db 61 GLYSLSSSVVTPSSSLGQTQYICWNNHKPSNTKDKKKVKEPKSCDKHTCPCPABELGG 120  
Qy 121 PSVFLPPKDKTMSRTPETCVVWDVSHEDEPVKFWYDGVIEVANVKTKREBQN 180  
Db 121 PSVFLPPKDKTMSRTPETCVVWDVSHEDEPVKFWYDGVIEVANVKTKREBQN 180  
Qy 181 STYRVVSLTVLHQMNNGKEYKCKVSNKALPAPIEKTISAKVOPREPOVYTLPSRDE 240  
Db 181 STYRVVSLTVLHQMNNGKEYKCKVSNKALPAPIEKTISAKVOPREPOVYTLPSRDE 240  
Qy 241 LTKNQVSLTCLVKGYFPSDIAVEMESNGOPENNYKTPPVLDVGSSFFLXSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGYFPSDIAVEMESNGOPENNYKTPPVLDVGSSFFLXSKLTVDKSRW 300  
Qy 301 QQGNVFSCSVNHEALTHYQKSLSLSPGK 330  
Db 301 QQGNVFSCSVNHEALTHYQKSLSLSPGK 330

US-09-899 949-38

Organism: Homo sapiens

Query Match 98.0%; Score 1729; DB 10; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLASSKSTSGGTAAAGLCLVKDYFPPVTWSWNSGALTSGVHTFPALLOSS 60  
Db 1 ASTKGPSVPLASSKSTSGGTAAAGLCLVKDYFPPVTWSWNSGALTSGVHTFPALLOSS 60

Qy 61 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120  
Db 1 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120

Qy 61 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120  
Db 1 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120

Qy 121 PSVFLFPKPDKDTMISRTPEVTCVWVVDVSHDPEVKFNWYDGVEVHNKTKPREQYN 180  
Db 121 PSVFLFPKPDKDTMISRTPEVTCVWVVDVSHDPEVKFNWYDGVEVHNKTKPREQYN 180

Qy 181 STYRVSVLTILHONWNGKEYKVKVSNALPAPIKTISAKVQPREQVITLPPSRDE 240  
Db 181 STYRVSVLTILHONWNGKEYKVKVSNALPAPIKTISAKVQPREQVITLPPSRDE 240

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWEENGOPENNYKTPPVLDVGSGFPLSKLTVDKSRW 300  
Db 241 LTKNOVSLTCLVKGFYPSDIAVEWEENGOPENNYKTPPVLDVGSGFPLSKLTVDKSRW 300

Qy 301 QGNVFSCSVMHEALTHNHYTOKSLSLSPGK 330  
Db 301 QGNVFSCSVMHEALTHNHYTOKSLSLSPGK 330

RESULT 5

US-10-047-542-20  
Sequence 20, Application US/10047542  
Publication No. US20020168367A1  
GENERAL INFORMATION:  
APPLICANT: LARICK, JAMES W.  
TITLE OF INVENTION: NOVEL IMMUNOADEHESINS FOR TREATING AND PREVENTING VIRAL  
TITLE OF INVENTION: AND BACTERIAL DISEASES  
FILE REFERENCE: 030905\_0004\_C1PL  
CURRENT APPLICATION NUMBER: US/10/047,542  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: PCT/US01/13932  
PRIOR FILING DATE: 2001-04-28  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 20  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-269-805-68

Query Match 98.0%; Score 1729; DB 14; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLASSKSTSGGTAAAGLCLVKDYFPPVTWSWNSGALTSGVHTFPALLOSS 60  
Db 1 ASTKGPSVPLASSKSTSGGTAAAGLCLVKDYFPPVTWSWNSGALTSGVHTFPALLOSS 60

Qy 61 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120  
Db 61 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120

Qy 121 PSVFLFPKPDKDTMISRTPEVTCVWVVDVSHDPEVKFNWYDGVEVHNKTKPREQYN 180  
Db 121 PSVFLFPKPDKDTMISRTPEVTCVWVVDVSHDPEVKFNWYDGVEVHNKTKPREQYN 180

Qy 181 STYRVSVLTILHONWNGKEYKVKVSNALPAPIKTISAKVQPREQVITLPPSRDE 240  
Db 181 STYRVSVLTILHONWNGKEYKVKVSNALPAPIKTISAKVQPREQVITLPPSRDE 240

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWEENGOPENNYKTPPVLDVGSGFPLSKLTVDKSRW 300  
Db 241 LTKNOVSLTCLVKGFYPSDIAVEWEENGOPENNYKTPPVLDVGSGFPLSKLTVDKSRW 300

Qy 301 QGNVFSCSVMHEALTHNHYTOKSLSLSPGK 330  
Db 301 QGNVFSCSVMHEALTHNHYTOKSLSLSPGK 330

RESULT 6

US-10-269-805-68  
Sequence 68, Application US/10269805  
Publication No. US20030124129A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN D.  
TITLE OF INVENTION: ANGIOPETIEN-2 SPECIFIC BINDING AGENTS  
FILE REFERENCE: A-772  
CURRENT APPLICATION NUMBER: US/10/269, 805  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/3728, 604  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 76  
SEQUENCE ID NO: 68  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-269-805-68

Query Match 98.0%; Score 1729; DB 14; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLASSKSTSGGTAAAGLCLVKDYFPPVTWSWNSGALTSGVHTFPALLOSS 60  
Db 1 ASTKGPSVPLASSKSTSGGTAAAGLCLVKDYFPPVTWSWNSGALTSGVHTFPALLOSS 60

Qy 61 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120  
Db 61 GLYSLSVVTVTPSSSLGGTGYTCINVNHKPSNTKVDKVKVPSCDKHTCPCPAPBLLGG 120

Qy 121 PSVFLFPKPDKDTMISRTPEVTCVWVVDVSHDPEVKFNWYDGVEVHNKTKPREQYN 180  
Db 121 PSVFLFPKPDKDTMISRTPEVTCVWVVDVSHDPEVKFNWYDGVEVHNKTKPREQYN 180

Qy 181 STYRVSVLTILHONWNGKEYKVKVSNALPAPIKTISAKVQPREQVITLPPSRDE 240  
Db 181 STYRVSVLTILHONWNGKEYKVKVSNALPAPIKTISAKVQPREQVITLPPSRDE 240

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWEENGOPENNYKTPPVLDVGSGFPLSKLTVDKSRW 300  
Db 241 LTKNOVSLTCLVKGFYPSDIAVEWEENGOPENNYKTPPVLDVGSGFPLSKLTVDKSRW 300

Qy 301 QGNVFSCSVMHEALTHNHYTOKSLSLSPGK 330  
Db 301 QGNVFSCSVMHEALTHNHYTOKSLSLSPGK 330

RESULT 7

US-10-310-719-8  
Sequence 8, Application US/10310719  
Publication No. US20030166163A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
FILE REFERENCE: IEX-020  
CURRENT APPLICATION NUMBER: US/10/310,719  
PRIOR APPLICATION NUMBER: 60/337,113  
PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 60/371,966  
 PRIOR FILING DATE: 2002-04-12  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 8  
 LENGTH: 330  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc  
 LOCATION: (1); (330)  
 OTHER INFORMATION: IgG1 constant region  
 US-10-310-719-8

Query Match 98.0%; Score 1729; DB 14; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVKGYPFPEPVTVSNNSGALTSGVHTFPAVLOSS 60  
 Db 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVKGYPFPEPVTVSNNSGALTSGVHTFPAVLOSS 60

Qy 61 GLYSLSSSWVTPSSGLGTOTYICNNHKSNTKVKVEKSKDCKTHCPCPAPELGG 120  
 Db 61 GLYSLSSSWVTPSSGLGTOTYICNNHKSNTKVKVEKSKDCKTHCPCPAPELGG 120

Qy 121 PSVFLPPKKDTLMISRPEVTCVVVDVSHEDPEVKWVYDGVEVHVKTKREEQVN 180  
 Db 121 PSVFLPPKKDTLMISRPEVTCVVVDVSHEDPEVKWVYDGVEVHVKTKREEQVN 180

Qy 121 PSVFLPPKKDTLMISRPEVTCVVVDVSHEDPEVKWVYDGVEVHVKTKREEQVN 180  
 Db 121 PSVFLPPKKDTLMISRPEVTCVVVDVSHEDPEVKWVYDGVEVHVKTKREEQVN 180

Qy 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240  
 Db 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240

Qy 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240  
 Db 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240

Qy 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240  
 Db 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240

Qy 241 LTKNQVSLTCLVKGYPFPSDIAVEMENGQEPENNYKTPPLDSGSFELYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGYPFPSDIAVEMENGQEPENNYKTPPLDSGSFELYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHEALTHNHYQORSLSLSPGK 330  
 Db 301 QQGNVFSCSVMHEALTHNHYQORSLSLSPGK 330

Qy 301 QQGNVFSCSVMHEALTHNHYQORSLSLSPGK 330  
 Db 301 QQGNVFSCSVMHEALTHNHYQORSLSLSPGK 330

RESULT 9  
 US-10-320-231A-81  
 Sequence 81, Application US/10370231A  
 Publication No. US20030194405A1  
 GENERAL INFORMATION:  
 APPLICANT: Neben, Steven  
 APPLICANT: Takeuchi, Toshihiko  
 APPLICANT: Tomkinson, Adrian  
 TITLE OF INVENTION: Treatment Of Asthma  
 FILE REFERENCE: 7430-163  
 CURRENT APPLICATION NUMBER: US/10/320,231A  
 PRIORITY APPLICATION NUMBER: US 60/342,174  
 PRIORITY FILING DATE: 2001-12-17  
 NUMBER OF SEQ ID NOS: 85  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 81  
 LENGTH: 330  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-320-231A-81

Query Match 98.0%; Score 1729; DB 14; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVKGYPFPEPVTVSNNSGALTSGVHTFPAVLOSS 60  
 Db 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVKGYPFPEPVTVSNNSGALTSGVHTFPAVLOSS 60

Qy 61 GLYSLSSSWVTPSSGLGTOTYICNNHKSNTKVKVEKSKDCKTHCPCPAPELGG 120  
 Db 61 GLYSLSSSWVTPSSGLGTOTYICNNHKSNTKVKVEKSKDCKTHCPCPAPELGG 120

Qy 121 PSVFLPPKKDTLMISRPEVTCVVVDVSHEDPEVKWVYDGVEVHVKTKREEQVN 180  
 Db 121 PSVFLPPKKDTLMISRPEVTCVVVDVSHEDPEVKWVYDGVEVHVKTKREEQVN 180

Qy 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240  
 Db 181 STYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPVYTIPPSRDE 240

Qy 241 LTKNQVSLTCLVKGYPFPSDIAVEMENGQEPENNYKTPPLDSGSFELYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGYPFPSDIAVEMENGQEPENNYKTPPLDSGSFELYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHEALTHNHYQORSLSLSPGK 330  
 Db 301 QQGNVFSCSVMHEALTHNHYQORSLSLSPGK 330

RESULT 10  
 US-10-383-902A-6 ;  
 Sequence 6, Application US/10383902A ;  
 Publication No. US2003022408A1 ;  
 GENERAL INFORMATION:  
 ; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus  
 ; APPLICANT: Mulberg, Juergen  
 ; APPLICANT: Lander, Robert C.  
 ; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY  
 ; FILE REFERENCE: 10280-04-2001  
 ; CURRENT APPLICATION NUMBER: US/10/383-902A  
 ; CURRENT FILING DATE: 2003-03-07  
 ; PRIOR APPLICATION NUMBER: US 6/362,403  
 ; PRIORITY FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetically generated plasmid sequence  
 ; US-10-383-902A-6

Query Match 98.0%; Score 1729; DB 15; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVTPSSSLGTQTYICNVNWKPSNTKVDKVKEPIKSCDKHTCPCPARBLGG 120  
 Db 61 GLYSLSVVTVTPSSSLGTQTYICNVNWKPSNTKVDKVKEPIKSCDKHTCPCPARBLGG 120

Qy 121 PSVFLFPKKPDOTLMSRTPEVTCVWVVDVSHEDPEVKFNNTYDGVEVNNTKTPRBEQYN 180  
 Db 121 PSVFLFPKKPDOTLMSRTPEVTCVWVVDVSHEDPEVKFNNTYDGVEVNNTKTPRBEQYN 180

Qy 181 STYRVSVLVTLYHQNMNGKEYKCKVSKNKAQKAKVQREPOVTTPLPSDE 240  
 Db 181 STYRVSVLVTLYHQNMNGKEYKCKVSKNKAQKAKVQREPOVTTPLPSDE 240

Qy 241 LTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTPPVIDSVESPPFLYPSKLTDKSRW 300  
 Db 241 LTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTPPVIDSVESPPFLYPSKLTDKSRW 300

Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330  
 Db 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 11  
 US-10-408-901-2  
 ; Sequence 2, Application US/10408901  
 ; Publication No. US2004022313A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Xu, Wenfeng  
 ; APPLICANT: No. US2004022313A1  
 ; APPLICANT: Whitmore, Theodore E.  
 ; APPLICANT: Grant, Francis J.  
 ; APPLICANT: Kindvogel, Wayne R.  
 ; APPLICANT: Klucher, Kevin M.  
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR  
 ; FILE REFERENCE: 02-10  
 ; CURRENT APPLICATION NUMBER: US/10/420,034A  
 ; CURRENT FILING DATE: 2003-04-18  
 ; PRIOR APPLICATION NUMBER: 60/373,813  
 ; NUMBER OF SEQ ID NOS: 69  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-420-034A-15

Query Match 98.0%; Score 1729; DB 15; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVTPSSSLGTQTYICNVNWKPSNTKVDKVKEPIKSCDKHTCPCPARBLGG 120  
 Db 61 GLYSLSVVTVTPSSSLGTQTYICNVNWKPSNTKVDKVKEPIKSCDKHTCPCPARBLGG 120

Qy 121 PSVFLFPKKPDOTLMSRTPEVTCVWVVDVSHEDPEVKFNNTYDGVEVNNTKTPRBEQYN 180

RESULT 13  
US-10-257-907-5  
; Sequence 5, Application US/10257907  
; Publication No. US20040043022A1  
; GENERAL INFORMATION:  
; APPLICANT: Heuer, Josef  
; APPLICANT: Liu, Jingi  
; APPLICANT: Na, Songgi  
; APPLICANT: Song, Ho Yeong  
; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY  
; FILE REFERENCE: X-13392  
; CURRENT APPLICATION NUMBER: US/10/257,907  
; CURRENT FILING DATE: 2002-10-16  
; NUMBER OF SEQ ID NOS: 5  
; SEQ ID NO 5  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-257-907-5

Query Match 98.0%; Score 1729; DB 15; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSPVFLAPSSKSTSGTAAGCLVQDYPPEPVTVNSGALTSGVHTPAVLOSS 60  
Db 1 ASTKGPSPVFLAPSSKSTSGTAALGCLVQDYPPEPVTVNSGALTSGVHTPAVLOSS 60

Qy 61 GLYSLSAVVTPVSSGLQTQYICNNHKSNTDKRKEFKSCDKTHCPCPAPELLGG 120  
Db 61 GLYSLSAVVTPVSSGLQTQYICNNHKSNTDKRKEFKSCDKTHCPCPAPELLGG 120

Qy 121 PSVFLPPKKDTLMSIRPTEPVTCVWVVDYSHEDPEVKFNYDGEVHNKTKEREEQYN 180  
Db 121 PSVFLPPKKDTLMSIRPTEPVTCVWVVDYSHEDPEVKFNYDGEVHNKTKEREEQYN 180

Qy 121 PSVFLPPKKDTLMSIRPTEPVTCVWVVDYSHEDPEVKFNYDGEVHNKTKEREEQYN 180  
Db 121 PSVFLPPKKDTLMSIRPTEPVTCVWVVDYSHEDPEVKFNYDGEVHNKTKEREEQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVTIPPSDE 240  
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVTIPPSDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSYMEALHNHYQRSLSLSPGK 330  
Db 301 QQGNVFSCSYMEALHNHYQRSLSLSPGK 330

RESULT 14  
US-10-656-769-2  
; Sequence 2, Application US/10656769  
; Publication No. US20040097712A1  
; GENERAL INFORMATION:  
; APPLICANT: Varnum, Brian

PRIOR APPLICATION NUMBER: US/03/892,949  
PRIOR FILING DATE: 2001-06-26  
CURRENT APPLICATION NUMBER: US 60/214,282  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 60/214,955  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/267,963  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 330  
LENGTH: 330  
TYPE: PRT

Query Match 98.0%; Score 1729; DB 15; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSPVFLAPSSKSTSGTAAGCLVQDYPPEPVTVNSGALTSGVHTPAVLOSS 60  
Db 1 ASTKGPSPVFLAPSSKSTSGTAALGCLVQDYPPEPVTVNSGALTSGVHTPAVLOSS 60

Qy 61 GLYSLSAVVTPVSSGLQTQYICNNHKSNTDKRKEFKSCDKTHCPCPAPELLGG 120  
Db 61 GLYSLSAVVTPVSSGLQTQYICNNHKSNTDKRKEFKSCDKTHCPCPAPELLGG 120

Qy 121 PSVFLPPKKDTLMSIRPTEPVTCVWVVDYSHEDPEVKFNYDGEVHNKTKEREEQYN 180  
Db 121 PSVFLPPKKDTLMSIRPTEPVTCVWVVDYSHEDPEVKFNYDGEVHNKTKEREEQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVTIPPSDE 240  
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVTIPPSDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSYMEALHNHYQRSLSLSPGK 330  
Db 301 QQGNVFSCSYMEALHNHYQRSLSLSPGK 330

RESULT 15  
US-10-772-531-38  
; Sequence 38, Application US/1072531  
; Publication No. US20040142422A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Preissel, Scott R.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Kuijper, Joseph L.  
; APPLICANT: Maurer, Mark F.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
; FILE REFERENCE: 00-42  
; CURRENT APPLICATION NUMBER: US/10/772,531  
; CURRENT FILING DATE: 2004-02-05  
; PRIOR APPLICATION NUMBER: US/03/892,949  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,282  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/214,955  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/267,963  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 330  
; LENGTH: 330  
; TYPE: PRT

; ORGANISM: Homo sapiens  
us-10-772-531-39

Query Match 98.0%; Score 1729; DB 16; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5.9e-126;  
Matches 323; Conservative 3; Missmatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPERVTWSNSGALTSGVHTPAVLOSS 60  
Db 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPERVTWSNSGALTSGVHTPAVLOSS 60

Qy 61 GLYSLSSSVTVTPSSSLGIGTQWICNWNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPBLGG 120  
Db 61 GLYSLSSSVTVTPSSSLGIGTQWICNWNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPBLGG 120

Qy 121 PSVFLPPKPKDITMISRTPEVTWVVDVSHEDPEYTKFNNWYDGVYEVHNVKTPREEQYN 180  
Db 121 PSVFLPPKPKDITMISRTPEVTWVVDVSHEDPEYTKFNNWYDGVYEVHNVKTPREEQYN 180

Qy 181 STYRVVSVLTLHQNWNGKEYCKVSKNKLAPIETKISKAKVQPREQYTLPSRDE 240  
Db 181 STYRVVSVLTLHQDWLNGKEYCKVSKNKLAPIETKISKAKGQPREQYTLPSRDE 240

Qy 241 LTKNQSLTCLVKGFPSDIAVEWESNGOPENNKYTTPVLDVSSEFFLYSKLTUDSRW 300  
Db 241 LTKNQSLTCLVKGFPSDIAVEWESNGOPENNKYTTPVLDVSSEFFLYSKLTUDSRW 300

Qy 301 QOGNVFSCSVMHEALINHYDORSLSSPGK 330  
Db 301 QOGNVFSCSVMHEALINHYDORSLSSPGK 330

Search completed: June 7, 2005, 09:25:06  
Job time : 145.767 secs

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US-08-236-311-7

Query Match 98.0%; Score 1729; DB 1; Length 371;

Best Local Similarity 97.9%; Pred. No. 3.2e-157; Mismatches 3; Indels 0; Gaps 0;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVLDKFPEPVTSWNAGALTSGHFTPAVLOSS 60

Db 42 ASTKGPSVFLAPSSKSTSGTAAAGCLVLDKFPEPVTSWNAGALTSGHFTPAVLOSS 101

QY 61 GLYSLSVVTPSSLGQTGYTICNYNHPKRENTKVKVVEPKSCDKTHTCPCPAPELGG 120

Db 102 GLYSLSVVTPSSLGQTGYTICNYNHPKRENTKVKVVEPKSCDKTHTCPCPAPELGG 161

QY 121 PSVLFPPKKDTLMISRTEVTCTVWDVSHEDEPKFVNWYDGVHNAKTKPREEQN 180

Db 162 PSVLFPPKKDTLMISRTEVTCTVWDVSHEDEPKFVNWYDGVHNAKTKPREEQN 221

QY 181 STYRVSVLTULHQMMGCKYCKVSNKALPAPIEKTISAKAQPREPQVYTLPPSRDE 240

Db 222 STYRVSVLTULHQMMGCKYCKVSNKALPAPIEKTISAKAQPREPQVYTLPPSRDE 281

QY 241 LTKNQVSLTCLVKGFTYPSDIAVEMESNGOPENNKTTPVLDGSFPLSFLVSKLTDKSRW 300

Db 282 LTKNQVSLTCLVKGFTYPSDIAVEMESNGOPENNKTTPVLDGSFPLSFLVSKLTDKSRW 341

QY 301 QOGNYFSCSVNHEALTHNHYQORSLSLSPGK 330

Db 342 QOGNYFSCSVNHEALTHNHYQORSLSLSPGK 371

RESULT 2  
US-08-437-918-7  
; Sequence 7, Application US/08457918  
; Patent No. 6117655  
; GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: KUDINEC, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0444P1C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 371 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-437-918-7

Query Match 98.0%; Score 1729; DB 3; Length 371;

Best Local Similarity 97.9%; Pred. No. 3.2e-157; Mismatches 3; Indels 0; Gaps 0;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLAPSSKSTSGTAAAGCLVLDKFPEPVTSWNAGALTSGHFTPAVLOSS 60

Db 42 ASTKGPSVFLAPSSKSTSGTAAAGCLVLDKFPEPVTSWNAGALTSGHFTPAVLOSS 101

QY 61 GLYSLSVVTPSSLGQTGYTICNYNHPKRENTKVKVVEPKSCDKTHTCPCPAPELGG 120

Db 102 GLYSLSVVTPSSLGQTGYTICNYNHPKRENTKVKVVEPKSCDKTHTCPCPAPELGG 161

QY 121 PSVLFPPKKDTLMISRTEVTCTVWDVSHEDEPKFVNWYDGVHNAKTKPREEQN 180

Db 162 PSVLFPPKKDTLMISRTEVTCTVWDVSHEDEPKFVNWYDGVHNAKTKPREEQN 221

QY 181 STYRVSVLTULHQMMGCKYCKVSNKALPAPIEKTISAKAQPREPQVYTLPPSRDE 240

Db 222 STYRVSVLTULHQMMGCKYCKVSNKALPAPIEKTISAKAQPREPQVYTLPPSRDE 281

QY 241 LTKNQVSLTCLVKGFTYPSDIAVEMESNGOPENNKTTPVLDGSFPLSFLVSKLTDKSRW 300

Db 282 LTKNQVSLTCLVKGFTYPSDIAVEMESNGOPENNKTTPVLDGSFPLSFLVSKLTDKSRW 341

QY 301 QOGNYFSCSVNHEALTHNHYQORSLSLSPGK 330

Db 342 QOGNYFSCSVNHEALTHNHYQORSLSLSPGK 371

RESULT 3  
US-10-157-408-7  
; Sequence 7, Application US/10157408  
; Patent No. 6710169  
; GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/157,408  
FILING DATE: 28-May-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: KUDINEC, Jeffrey S.

APPLICATION NUMBER: 07/936190

.

FILING DATE: 26-AUG-1992  
 APPLICATION NUMBER: 07/842777  
 FILING DATE: 18-FEB-1992  
 APPLICATION NUMBER: 07/250785  
 FILING DATE: 28-SEP-1988  
 APPLICATION NUMBER: 07/104329  
 FILING DATE: 02-OCT-1987  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kubinec, Jeffrey S.  
 REGISTRATION NUMBER: 36,575  
 REFERENCE/DOCKET NUMBER: P0444P1C3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-8228  
 TELEFAX: 415/952-9881  
 TELEX: 9101371-7168  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 371 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 ; US-10-157-408-7

Query Match 98.0%; Score 1729; DB 4; Length 371;  
 Best Local Similarity 97.9%; Pred. No. 3.2e-157;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKTSKSGTAAAGCLVKDVKYFPERTVWSNSGALTSGVHTFPAVLOSS 60  
 Db 42 ASTKGPSVFLPAPSSKTSKSGTAAAGCLVKDVKYFPERTVWSNSGALTSGVHTFPAVLOSS 101

Qy 61 GLYSLSVVTVPPSSSLGTOTVICNWNHKPSNTKVDKVKEPKSCDKHTCPCPAPLLGG 120  
 Db 102 GLYSLSVVTVPPSSSLGTOTVICNWNHKPSNTKVDKVKEPKSCDKHTCPCPAPLLGG 161

Qy 121 PSVFLPPKPKDTLMISRTPETVTVVVDVSIRHEDPEVKFNWTVGDVEVHNWKTKPREGYN 180  
 Db 162 PSVFLPPKPKDTLMISRTPETVTVVVDVSIRHEDPEVKFNWTVGDVEVHNWKTKPREGYN 221

Qy 181 STYRVVSVLTVLHQINMNGKEYKCKVSKNKAAPAKTISAKVOPREPOVTLPSPRDE 240  
 Db 222 STYRVVSVLTVLHQDLNGKEYKCKVSKNKAAPAKTISAKVOPREPOVTLPSPRDE 281

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDVGSPFLYIKLTVDSKRW 300  
 Db 282 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDVGSPFLYIKLTVDSKRW 341

Qy 301 QOGNVFSCSVWHEALINHYQORSLSLSPGK 330  
 Db 342 QOGNVFSCSVWHEALINHYQORSLSLSPGK 371

RESULT<sup>4</sup>  
 ; Sequence 7, Application US/08397411.  
 ; Patent No. 6129914  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weinrich, George  
 ; APPLICANT: Gingrich, Roger  
 ; APPLICANT: Link, Brian  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
 ; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: Townsend and Townsend and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08397,411  
 FILING DATE: 01-MAR-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/859, 583  
 FILING DATE: 27-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M.  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 011823-004901  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-26-2422  
 TELEFAX: 415-952-9881  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 446 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ; US-08-397-411-7

Query Match 98.0%; Score 1729; DB 3; Length 446;  
 Best Local Similarity 97.9%; Pred. No. 4.2e-157;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLPAPSSKTSKSGTAAAGCLVKDVKYFPERTVWSNSGALTSGVHTFPAVLOSS 60  
 Db 117 ASTKGPSVFLPAPSSKTSKSGTAAAGCLVKDVKYFPERTVWSNSGALTSGVHTFPAVLOSS 176

Qy 61 GLYSLSVVTVPPSSSLGTOTVICNWNHKPSNTKVDKVKEPKSCDKHTCPCPAPLLGG 120  
 Db 177 GLYSLSVVTVPPSSSLGTOTVICNWNHKPSNTKVDKVKEPKSCDKHTCPCPAPLLGG 236

Qy 121 PSVFLPPKPKDTLMISRTPETVTVVVDVSIRHEDPEVKFNWTVGDVEVHNWKTKPREGYN 180  
 Db 237 PSVFLPPKPKDTLMISRTPETVTVVVDVSIRHEDPEVKFNWTVGDVEVHNWKTKPREGYN 296

Qy 181 STYRVVSVLTVLHQINMNGKEYKCKVSKNKAAPAKTISAKVOPREPOVTLPSPRDE 240  
 Db 297 STYRVVSVLTVLHQDLNGKEYKCKVSKNKAAPAKTISAKVOPREPOVTLPSPRDE 356

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDVGSPFLYIKLTVDSKRW 300  
 Db 357 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDVGSPFLYIKLTVDSKRW 416

Qy 301 QOGNVFSCSVWHEALINHYQORSLSLSPGK 330  
 Db 417 QOGNVFSCSVWHEALINHYQORSLSLSPGK 446

RESULT<sup>5</sup>  
 ; Sequence 13, Application US/08458516  
 ; Sequence 13, Application US/08458516  
 ; Patent No. 5777085  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co, Man Sung  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with  
 ; TITLE OF INVENTION: GPIIB/IIIA  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: William M. Smith  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:

RESULT 6  
US-08-030-175-41  
; Sequence 41, Application US/08030175  
; Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.

RESULT 6  
US-08-030-175-41  
; Sequence 41, Application US/08030175  
; Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.

RESULT 6  
US-08-030-175-41  
; Sequence 41, Application US/08030175  
; Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.

RESULT 6  
US-08-030-175-41  
; Sequence 41, Application US/08030175  
; Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.

RESULT 6  
US-08-030-175-41  
; Sequence 41, Application US/08030175  
; Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: WordPerfect 5.0 (Dos Text)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE: 03-MAY-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;  
Matches 321; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ASTKGPSPVFLAPSSKSTSGTAAIGCLVLDYFPEPVTVWSNAGLTSGVHTFPVLOSS 60  
Db 120 ASTKGPSPVFLAPSSKSTSGTAAIGCLVLDYFPEPVTVWSNAGLTSGVHTFPVLOSS 179  
Qy 61 GLYSLSVVTPSSIGTQYICINWINKHSNTKDKVKVEPKSCDKHTCPCPABLLGG 120  
Db 180 GLYSLSVVTPSSIGTQYICINWINKHSNTKDKVKVEPKSCDKHTCPCPABLLGG 239  
Qy 121 PSVFLPPPKDTLMISRTPEVTCVVWDVSHEDPEVKFNWVDG/EVNWKTKPREEQYN 180  
Db 240 PSVFLPPPKDTLMISRTPEVTCVVWDVSHEDPEVKFNWVDG/EVNWKTKPREEQYN 299  
Qy 181 STYRVVSVLTVLHQWNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
Db 300 STYRVVSVLTVLHQWNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 359  
Qy 241 LTKQVSLSITLVKGYPSDIAVEMWSNGOPENNYKTPPLDSGSFELYSKLTDKSRW 300  
Db 360 LTKQVSLSITLVKGYPSDIAVEMWSNGOPENNYKTPPLDSGSFELYSKLTDKSRW 419  
Qy 301 QQGNVFSCSYWHEALHNHYQSLISLSPGK 330  
Db 420 QQGNVFSCSYWHEALHNHYQSLISLSPGK 449

Query Match 98.0%; Score 1729; DB 4; Length 467;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ASTKGPSPVFLAPSSKSTSGTAAIGCLVLDYFPEPVTVWSNAGLTSGVHTFPVLOSS 60  
Db 138 ASTKGPSPVFLAPSSKSTSGTAAIGCLVLDYFPEPVTVWSNAGLTSGVHTFPVLOSS 197  
Qy 61 GLYSLSVVTPSSIGTQYICINWINKHSNTKDKVKVEPKSCDKHTCPCPABLLGG 120  
Db 198 GLYSLSVVTPSSIGTQYICINWINKHSNTKDKVKVEPKSCDKHTCPCPABLLGG 257  
Qy 121 PSVFLPPPKDTLMISRTPEVTCVVWDVSHEDPEVKFNWVDG/EVNWKTKPREEQYN 180  
Db 258 PSVFLPPPKDTLMISRTPEVTCVVWDVSHEDPEVKFNWVDG/EVNWKTKPREEQYN 317  
Qy 181 STYRVVSVLTVLHQWNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
Db 318 STYRVVSVLTVLHQWNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 377  
Qy 241 LTKQVSLSITLVKGYPSDIAVEMWSNGOPENNYKTPPLDSGSFELYSKLTDKSRW 300  
Db 378 LTKQVSLSITLVKGYPSDIAVEMWSNGOPENNYKTPPLDSGSFELYSKLTDKSRW 437  
Qy 301 QQGNVFSCSYWHEALHNHYQSLISLSPGK 330  
Db 438 QQGNVFSCSYWHEALHNHYQSLISLSPGK 467

Query Match 98.0%; Score 1729; DB 4; Length 467;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ASTKGPSPVFLAPSSKSTSGTAAIGCLVLDYFPEPVTVWSNAGLTSGVHTFPVLOSS 60  
Db 138 ASTKGPSPVFLAPSSKSTSGTAAIGCLVLDYFPEPVTVWSNAGLTSGVHTFPVLOSS 197  
Qy 61 GLYSLSVVTPSSIGTQYICINWINKHSNTKDKVKVEPKSCDKHTCPCPABLLGG 120  
Db 198 GLYSLSVVTPSSIGTQYICINWINKHSNTKDKVKVEPKSCDKHTCPCPABLLGG 257  
Qy 121 PSVFLPPPKDTLMISRTPEVTCVVWDVSHEDPEVKFNWVDG/EVNWKTKPREEQYN 180  
Db 258 PSVFLPPPKDTLMISRTPEVTCVVWDVSHEDPEVKFNWVDG/EVNWKTKPREEQYN 317  
Qy 181 STYRVVSVLTVLHQWNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
Db 318 STYRVVSVLTVLHQWNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 377  
Qy 241 LTKQVSLSITLVKGYPSDIAVEMWSNGOPENNYKTPPLDSGSFELYSKLTDKSRW 300  
Db 378 LTKQVSLSITLVKGYPSDIAVEMWSNGOPENNYKTPPLDSGSFELYSKLTDKSRW 437  
Qy 301 QQGNVFSCSYWHEALHNHYQSLISLSPGK 330  
Db 438 QQGNVFSCSYWHEALHNHYQSLISLSPGK 467

COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: WordPerfect 5.0 (DOS Text)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.

REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

; US-08-030-175-42

Query Match 98 %; Score 1729; DB 4; Length 467;  
Best Local Similarity 97.9%; Pred. No. 4.5e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPERVTWSSNSGALTSGVHTFPAVLQSS 60  
Db 138 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPERVTWSSNSGALTSGVHTFPAVLQSS 197  
Qy 61 GLYSLSVVTVPPSSGLTQWVNCNNHAKPSNTKVDKVKEPKSCDKHTCPCPARLIGG 120  
Db 198 GLYSLSVVTVPPSSGLTQWVNCNNHAKPSNTKVDKVKEPKSCDKHTCPCPARLIGG 257  
Qy 121 PSVFLFPKPDKTLMISRTPETVTVWVDSHEDPEVKFNWVDDGVFVNNTKPRBEQYN 180  
Db 258 PSVFLFPKPDKTLMISRTPETVTVWVDSHEDPEVKFNWVDDGVFVNNTKPRBEQYN 317  
Qy 181 STYRVISVLTVLHQNMNGKEYKCKVSKNKAPEAKTISKAKVOPREPOVTLPSRDE 240  
Db 318 STYRVISVLTVLHQDWLNGKEYKCKVSKNKAPEAKTISKAKGOPREPOVTLPSRDE 377  
Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDGSVSPFLYSLKLTVDKSRW 300  
Db 378 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDGSFPLYSLKLTVDKSRW 437  
Qy 301 QQGNVFSCSVNHEALHNHYQRSLSLSPGK 330  
Db 438 QQGNVFSCSVNHEALHNHYQRSLSLSPGK 467

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/1952640  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1808-118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

; US-08-378-939-10

Query Match 98 %; Score 1729; DB 2; Length 476;  
Best Local Similarity 97.9%; Pred. No. 4.7e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPERVTWSSNSGALTSGVHTFPAVLQSS 60  
Db 147 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPERVTWSSNSGALTSGVHTFPAVLQSS 206  
Qy 61 GLYSLSVVTVPPSSGLTQWVNCNNHAKPSNTKVDKVKEPKSCDKHTCPCPARLIGG 120  
Db 207 GLYSLSVVTVPPSSGLTQWVNCNNHAKPSNTKVDKVKEPKSCDKHTCPCPARLIGG 266  
Qy 121 PSVFLFPKPDKTLMISRTPETVTVWVDSHEDPEVKFNWVDDGVFVNNTKPRBEQYN 180  
Db 267 PSVFLFPKPDKTLMISRTPETVTVWVDSHEDPEVKFNWVDDGVFVNNTKPRBEQYN 326  
Qy 181 STYRVISVLTVLHQNMNGKEYKCKVSKNKAPEAKTISKAKVOPREPOVTLPSRDE 240  
Db 327 STYRVISVLTVLHQDWLNGKEYKCKVSKNKAPEAKTISKAKGOPREPOVTLPSRDE 386  
Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDGSVSPFLYSLKLTVDKSRW 300  
Db 387 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDGSFPLYSLKLTVDKSRW 446  
Qy 301 QQGNVFSCSVNHEALHNHYQRSLSLSPGK 330  
Db 447 QQGNVFSCSVNHEALHNHYQRSLSLSPGK 476

RESULT 8  
US-08-378-939-10  
Sequence 10, Application US/08378939  
Patent No. 587961  
GENERAL INFORMATION:  
APPLICANT: CROWE, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROTHWEIL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.

RESULT 9  
US-09-746-359A-54  
Sequence 54, Application US/09746359A  
Patent No. 6510286  
GENERAL INFORMATION:  
APPLICANT: Thompson, Penny  
APPLICANT: Foster, Donald C.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Madden, Karen L.  
APPLICANT: Kelly, James D.  
APPLICANT: Sprache, Cindy A.  
APPLICANT: Blumberg, Hal  
APPLICANT: Eagan, Maribeth A.  
APPLICANT: Jasper, Stephen R.  
APPLICANT: Chandrasekher, Yasmin A.  
APPLICANT: No. 6610286ak, Julia E.

TITLE OF INVENTION: Method for Treating Inflammation  
FILE REFERENCE: 99-08  
CURRENT APPLICATION NUMBER: US/09/746,359A  
PRIORITY FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/171,969  
PRIOR FILING DATE: 1999-12-23  
PRIORITY APPLICATION NUMBER: 2000-06-22  
NUMBER OF SEQ ID NOS.: 72  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO: 54  
LENGTH: 547  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-746-359A-54

Query Match 98.0%; Score 1729; DB 4; Length 547;  
Best Local Similarity 97.9%; Pred. No. 5.1e-157; Mismatches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Matches 323;

Qy 1 ASTKGPSPVFLAPSSKSTSGCTAALGCLVVDYFEPRTVWSNSGALTSGWHTPAVLSS 60  
Db 238 ASTKGPSPVFLAPSSKSTSGCTAALGCLVVDYFEPRTVWSNSGALTSGWHTPAVLSS 60

Qy 61 GLYSLSVVVPSSSLGTQTYICNWKPSNTKVKVPSKCDKTHTCPPCPABELGG 120  
Db 278 GLYSLSVVVPSSSLGTQTYICNWKPSNTKVKVPSKCDKTHTCPPCPABELGG 120

Qy 121 PSVFLFPPKKDKDTLMSRTEPVTCVVWDVSHEDPEVKFNWYDGVEVHNKTKPREEQYN 180  
Db 338 PSVFLFPPKKDKDTLMSRTEPVTCVVWDVSHEDPEVKFNWYDGVEVHNKTKPREEQYN 180

Qy 181 STYRVSVLTUHQWMNGKEYCKVSKNKLPAPEKTIKAKVOPREPOVYTLPPSDE 240  
Db 398 STYRVSVLTUHQDLNGKEYCKVSKNKLPAPEKTIKAKGOPREPOVYTLPPSDE 457

Qy 61 GLYSLSVVVPSSSLGTQTYICNWKPSNTKVKVPSKCDKTHTCPPCPABELGG 120  
Db 458 LTKNQVSLTCLVKGFTPSDAVEWSNGQPNNYKTPPLDSVSFFLJKLTVDKSRW 517

Qy 301 QQGNVFSCSYVHEALHNHYQQRSLSPGK 330  
Db 301 QQGNVFSCSYVHEALHNHYQQRSLSPGK 330

Qy 538 QQGNVFSCSYVHEALHNHYQQRSLSPGK 567  
Db 518 QQGNVFSCSYVHEALHNHYQQRSLSPGK 547

---

RESULT 11  
US-09-746-359A-53

Sequence 53, Application US/09746359A  
; Sequence 53, Application US/09746359A  
; Patent No. 6610286

GENERAL INFORMATION:

APPLICANT: Thompson, Penny  
APPLICANT: Foster, Donald C.  
APPLICANT: Xu, Wenfang  
APPLICANT: Madden, Karen L.  
APPLICANT: Kelly, James D.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Blumberg, Hal  
APPLICANT: Bagan, Maribeth A.  
APPLICANT: Jaspers, Stephen R.  
APPLICANT: Chandrasekher, Yasmin A.  
APPLICANT: No. 6610286A  
APPLICANT: No. 6610286A  
APPLICANT: No. 6610286A

TITLE OF INVENTION: Method for Treating Inflammation  
FILE REFERENCE: 99-08  
CURRENT APPLICATION NUMBER: US/09/746,359A  
PRIORITY FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/171,969  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/213,341  
PRIOR FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS.: 72  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO: 53  
LENGTH: 571  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-746-359A-53

Query Match 98.0%; Score 1729; DB 4; Length 571;  
Best Local Similarity 97.9%; Pred. No. 6.1e-157; Mismatches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Matches 323;

Qy 1 ASTKGPSPVFLAPSSKSTSGCTAALGCLVVDYFEPRTVWSNSGALTSGWHTPAVLSS 60  
Db 242 ASTKGPSPVFLAPSSKSTSGCTAALGCLVVDYFEPRTVWSNSGALTSGWHTPAVLSS 60

Qy 61 GLYSLSVVVPSSSLGTQTYICNWKPSNTKVKVPSKCDKTHTCPPCPABELGG 120  
Db 302 GLYSLSVVVPSSSLGTQTYICNWKPSNTKVKVPSKCDKTHTCPPCPABELGG 361

Qy 121 PSVFLPPPKDQTLMSRTPEVTCVWDVSHEDEPKFNMVYDGIVHNVTKPREGYN 180  
 Db 362 PSVFLPPPKDQTLMSRTPEVTCVWDVSHEDEPKFNMVYDGIVHNVTKPREGYN 421  
 Qy 181 STYRVVSVLTVLHQDWLNGKEYKCKVSKNKLAPAPIEKTISAKVOPREPQVTLPSPRDE 240  
 Db 422 STYRVVSVLTVLHQDWLNGKEYKCKVSKNKLAPAPIEKTISAKVOPREPQVTLPSPRDE 481  
 Qy 241 LTKNOVSLTCLVKGFPSDAVEWSNGOPENNYKTPPVLDVSFELVKLTVDSRW 300  
 Db 482 LTKNOVSLTCLVKGFPSDAVEWSNGOPENNYKTPPVLDVSFELVKLTVDSRW 541  
 Qy 301 QQGNVFSCSVMEALINHYQORSLSLSPGK 330  
 Db 542 QQGNVFSCSVMEALINHYQORSLSLSPGK 571

RESULT 12  
 US-09-313-942-9  
 ; Sequence 9, Application US/09313942  
 ; Patent No. 6472179  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; TITLE OF INVENTION: AND USE  
 ; FILE REFERENCE: REG 203-A  
 ; CURRENT APPLICATION NUMBER: US/09/313, 942  
 ; CURRENT FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 09/313, 942  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR FILING DATE: 1998-09-25  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 9  
 ; LENGTH: 951  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-313-942-9

Query Match 98.0%; Score 1729; DB 4; Length 951;  
 Best Local Similarity 97.9%; Pred. No. 1.3e-156;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLPAPSSKRSTSGTAAGLCLVVDYFPEPVTVWSNGALTSGVHTFPAVLQS 60  
 Db 133 ASTKGPSVFLPAPSSKRSTSGTAAGLCLVVDYFPEPVTVWSNGALTSGVHTFPAVLQS 192  
 Qy 61 GLYSIASSWVTPSSLLGTOTYICNTNHKPNTRKVKVKEKSCDKHTCPCPAPBLGG 120  
 Db 193 GLYSIASSWVTPSSLLGTOTYICNTNHKPNTRKVKVKEKSCDKHTCPCPAPBLGG 252  
 Qy 121 PSVFLPPPKDQTLMSRTPEVTCVWDVSHEDEPKFNMVYDGIVHNVTKPREGYN 180  
 Db 253 PSVFLPPPKDQTLMSRTPEVTCVWDVSHEDEPKFNMVYDGIVHNVTKPREGYN 312  
 Qy 181 STYRVVSVLTVLHQDWLNGKEYKCKVSKNKLAPAPIEKTISAKVOPREPQVTLPSPRDE 240  
 Db 313 STYRVVSVLTVLHQDWLNGKEYKCKVSKNKLAPAPIEKTISAKVOPREPQVTLPSPRDE 372  
 Qy 241 LTKNOVSLTCLVKGFPSDAVEWSNGOPENNYKTPPVLDVSFELVKLTVDSRW 300  
 Db 373 LTKNOVSLTCLVKGFPSDAVEWSNGOPENNYKTPPVLDVSFELVKLTVDSRW 432  
 Qy 301 QQGNVFSCSVMEALINHYQORSLSLSPGK 330  
 Db 433 QQGNVFSCSVMEALINHYQORSLSLSPGK 462

RESULT 14  
 US-09-740-002-27  
 ; Sequence 27, Application US/09740002  
 ; Patent No. 6537809  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BRAAMS, PETER  
 ; APPLICANT: MORROW, PHILLIP  
 ; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
 ; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
 ; FILE REFERENCE: 037003217575  
 ; CURRENT APPLICATION NUMBER: US/09/740, 002  
 ; CURRENT FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: 09/315, 697  
 ; PRIOR FILING DATE: 1999-06-18  
 ; PRIOR APPLICATION NUMBER: 08/488, 376  
 ; PRIOR FILING DATE: 1995-06-07  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 27  
 ; LENGTH: 475  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-740-002-27

RESULT 13  
 US-09-289-942A-7  
 ; Sequence 7, Application US/09289942A

Query Match 97.8%; Score 1725; DB 4; Length 475;  
 Best Local Similarity 97.6%; Pred. No. 1.1e-156;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0;  
 Gaps 0; Patents 322; Conservative 3; Mismatches 5; Indels 0;  
 Gaps 0; Mismatches 3; Indels 0; Gaps 0;

Query	DB	Query	DB
QY 1 ASTKQPSVFLAPSSKSTSGTAAAGCLVDRYFPEPVTVWSNGLTSQHTRPAVLOSS	QY 1 ASTKQPSVFLAPSSKSTSGTAAAGCLVDRYFPEPVTVWSNGLTSQHTRPAVLOSS		
Db 146 ASTKQPSVFLAPSSKSTSGTAAAGCLVDRYFPEPVTVWSNGLTSQHTRPAVLOSS 60	Db 147 ASTKQPSVFLAPSSKSTSGTAAAGCLVDRYFPEPVTVWSNGLTSQHTRPAVLOSS 205		
QY 61 GLYSASSWVTPSSSLGQTQYICNNHKSNTKDKKQFERSCOKHTCPCPAPELGG 120	QY 61 GLYSASSWVTPSSSLGQTQYICNNHKSNTKDKKQFERSCOKHTCPCPAPELGG 120		
Db 206 GLYSASSWVTPSSSLGQTQYICNNHKSNTKDKKQFERSCOKHTCPCPAPELGG 265	Db 207 GLYSASSWVTPSSSLGQTQYICNNHKSNTKDKKQFERSCOKHTCPCPAPELGG 265		
QY 121 PSVFLPPKKDTLMISRTEPVTCVVVDYSHEDPEVKFWYVDSGVENHKTKRREQIN 180	QY 121 PSVFLPPKKDTLMISRTEPVTCVVVDYSHEDPEVKFWYVDSGVENHKTKRREQIN 180		
Db 266 PSVFLPPKKDTLMISRTEPVTCVVVDYSHEDPEVKFWYVDSGVENHKTKRREQIN 325	Db 267 PSVFLPPKKDTLMISRTEPVTCVVVDYSHEDPEVKFWYVDSGVENHKTKRREQIN 325		
QY 181 STYRVSVLVTLHQNMNGKEYKCKVSNKALPAPIEKTISAKQPREPOVYTLLPSRDE 240	QY 181 STYRVSVLVTLHQNMNGKEYKCKVSNKALPAPIEKTISAKQPREPOVYTLLPSRDE 240		
Db 326 STYRVSVLVTLHQMLNGKEYKCKVSNKALPAPIEKTISAKQPREPOVYTLLPSRDE 385	Db 327 STYRVSVLVTLHQMLNGKEYKCKVSNKALPAPIEKTISAKQPREPOVYTLLPSRDE 385		
QY 241 LTQNQVSITCLVKGYFPSDIAVENSNGQEPENNKTTPVLDGSFFLUSKLTKDSRW 300	QY 241 LTQNQVSITCLVKGYFPSDIAVENSNGQEPENNKTTPVLDGSFFLUSKLTKDSRW 300		
Db 386 LTQNQVSITCLVKGYFPSDIAVENSNGQEPENNKTTPVLDGSFFLUSKLTKDSRW 445	Db 387 LTQNQVSITCLVKGYFPSDIAVENSNGQEPENNKTTPVLDGSFFLUSKLTKDSRW 445		
QY 301 QQGNVFSCSVMHEALHNHYQKSLSLSPGK 330	QY 301 QQGNVFSCSVMHEALHNHYQKSLSLSPGK 330		
Db 446 QQGNVFSCSVMHEALHNHYQKSLSLSPGK 475	Db 447 QQGNVFSCSVMHEALHNHYQKSLSLSPGK 476		

RESULT 15  
 US-08-487-550-4  
 Sequence 4, Application US/08487550  
 Patent No. 611398  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, Darrell R.  
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
 TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 STREET: 699 Prince Street  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22314  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,550  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Takin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-131  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 476 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-487-550-4

Query Match 97.8%; Score 1725; DB 3; Length 476;  
 Best Local Similarity 97.6%; Pred. No. 1.1e-155; Length 476;

Search completed: June 7, 2005, 09:04:00  
 Job time : 47.1658 secs

GenCore version 5.1.6  
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### OM protein - protein search, using SW model

Run on: June 7, 2005, 08:48:08 ; Search time 24.4421 Seconds  
 (without alignments)  
 913.271 Million cell updates/sec

Title: US-10-000-439-3  
 Perfect score: 1260  
 Sequence: 1 EPKSCDKTHICPPCPAPEL.....MHEALHNHYQORSLISLSPGK 232  
 Scoring table: Blosum62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96215763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79;\*  
 1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1225	97.2	330	1	GHHU
2	1219	96.7	374	2	Ig gamma-1 chain C region - human
3	1217	96.6	255	4	C;Species: Homo sapiens (man)
4	1172	93.0	234	2	C;Date: 31-Jan-1981 #sequence revision 18-Aug-1992 #text change 09-Jul-2004
5	1138	90.3	377	2	C;Accession: A93433; S3881; S3887; B90563; A90564; B91668; A91723; A02146
6	1136	90.2	377	2	R;Ellison, J.W.; Benson, B.J.; Hood, L.E.
7	1123	89.1	289	1	Nucleic Acids Res. 10, 4071-4079, 1982
8	1107	87.9	326	1	A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
9	1097	87.1	327	1	A;Reference number: A93433; MUID:82274238; PMID:6287432
10	883	70.1	323	1	A;Accession: A93433
11	868.5	68.9	328	2	A;Molecule type: DNA
12	868.5	68.9	328	2	A;Cross-references: EMBL:Z17370
13	865	68.7	277	2	R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
14	858	68.1	329	1	Cell 29, 671-679, 1982
15	847.5	67.3	328	2	A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a class of genes.
16	840.5	66.7	328	2	A;Reference number: S33887; MUID:33001543; PMID:6811339
17	820	65.1	147150		A;Accession: S33887
18	813	64.5	333	2	A;Molecule type: DNA
19	812.5	64.5	326	2	A;Residues: 88-113/235-330 <PAK>
20	811.5	64.4	308	2	A;Cross-references: EMBL:Z17370
21	811.5	64.4	472	2	R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.
22	801.5	63.6	398	1	A;Title: The covalent structure of a human gammag-immunoglobulin. VII. Amino acid sequences.
23	794.5	63.1	444	2	A;Reference number: A90563; MUID:71064024; PMID:5489771
24	789.5	62.7	324	1	A;Contents: myeloma Eu
25	784.5	62.3	326	2	A;Molecule type: protein
26	784.5	62.3	393	1	R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
27	776.5	61.6	329	2	A;Biocatalysis 9, 3171-3181, 1970
28	776	61.6	330	1	A;Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequencer
29	61.6	46.9	2	R;Ponstingl, H.; Hilschmann, N.	
29	61.6	46.9	2	Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976	
29	61.6	46.9	2	A;Title: Die Primaerstruktur eines monoklonalen IgG1-immunglobulins (Myelomprotein Nie),	

Score	Length	DB ID	Description
30	772	61.3	Ig gamma-2a chain
31	771	61.2	Ig gamma-2a chain
32	761	60.4	Ig gamma-2b chain
33	751.5	59.6	Ig gamma-2b chain
34	747.5	59.3	Ig gamma-2b chain
35	746.5	59.2	Ig gamma-2b chain
36	735	58.3	Ig gamma-2 chain C
37	731.5	58.1	Ig gamma-2b chain
38	669	53.1	Ig gamma heavy chain
39	549	43.6	Ig heavy chain VH1
40	547	43.4	Ig heavy chain V-I
41	542	43.0	Ig gamma-1 chain C
42	366.5	29.1	Ig gamma-1 chain (
43	357	28.3	Ig heavy chain pre
44	353	28.0	Ig mu chain C regi
45	353	28.0	Ig mu chain C regi

### ALIGNMENTS

igen Primärstruktur.

A; Reference number: A91668; MUID:77070269; PMID:826475

A; Contents: myeloma protein Nie

A; Accession: B91668

A; Molecule type: protein

A; Residues: 1-34, Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'B', 27

A; Note: this sequence has the Gim(17) and Gim(1) markers

R. Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A; Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL

A; Reference number: A91723; MUID:83289131; PMID:6884994

A; Contents: myeloma protein KOL; disulfide bonds

A; Accession: A91723

A; Molecule type: protein

A; Residues: 1-96, R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <sch>

A; Note: this sequence has the Gim(3) and Gim(non-1) markers

R.Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide

A; Reference number: A90565; MUID:71064027; PMID:493144

A; Contents: annotation; disulfide bonds

R; Breker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

endromic cleavage products, and the disulfide bridges

A; Reference number: A91667; MUID:77070267; PMID:1002129

A; Contents: annotation; disulfide bonds

C; Genetics:

A; Gene: GDB:1CHG1

A; Cross-references: GDB:120085; OMIM:147100

A; Map position: 14q32.3-14q22.33

A; Introns: 99/1; 114/1; 224/1

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κα)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F; 20-85/Domain: immunoglobulin homology <IM3>

F; 243-310/Domain: immunoglobulin homology <IM2>

F; 27-83/144-204, 250-308/Disulfide bonds: #status experimental

F; 103/Disulfide bonds: interchain (to light chain) #status experimental

F; 109-112/Disulfide bonds: interchain (to heavy chain) #status experimental

F; 180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.2%; Score 1225; DB 1; Length 330;

Best Local Similarity 97.0%; Pred. No. 3.5e-85; 4; Mismatches 0; Indels 0; Gaps 0;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

### RESULT 3

S31866

19 gamma-1 chain C region - synthetic

C; Species: synthetic

A; Note: Homo Sapiens (man) gene engineered and expressed in Escherichia coli

C; Accession: S31866

R; Filipula, D.

submitted to the EMBL Data library, February 1993

A; Description: Screening method for protein-protein interactions of cloned gene products.

A; Reference number: S31866

A; Accession: S31866

A; Molecule type: mRNA

A; Residues: 1-255 <FILE>

A; Cross-references: EMBL:X70421; NID:933068; PIDN:CAA49866.1; PID:933069

C; Keywords: immunoglobulin

F; 1-22/Region: Bacteriophaga coli outer membrane protein A precursor

F; 23-255/Region: human Ig gamma-1 chain C region

Query Match 96.6%; Score 1217; DB 4; Length 255;

Best Local Similarity 96.6%; Pred. No. 1e-84; 5; Mismatches 0; Indels 0; Gaps 0;

Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 2

S6339

Ig heavy chain V region precursor - human

C; Species: Homo Sapiens (man)

C; Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

C; Accession: S69339; S77664

R; Khamlichchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Bio. J. Biochem. 229, 54-60, 1995

A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A; Reference number: S69339; MUID:95262687; PMID:7744049

A; Accession: S69339

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-374 <KHA>

A; Cross-references: EMBL:X81695

R; Khamlichchi, A.A.

submitted to the EMBL Data Library, September 1994

A; Reference number: S72664

A; Accession: S72664

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-140, 'C', 142-374 <KH2>

A; Cross-references: EMBL:X81695

C; Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 96.1%; Score 1219; DB 2; Length 374;

Best Local Similarity 96.1%; Pred. No. 1.2e-84; 4; Mismatches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 143 EPKSDCKTHCPCCPAPELGGPSVLFPPKPKOTLMISRTPEVCVVVDVSHDPEVK 60

Qy 61 NWYVGDGVENVNVKTKPREGQSYNTVRVSVLTVLHQNWNGKEYKCKVSNKALPAIETK 120

Db 203 NWYVGDGVENVNVAKTKPREGQSYNTVRVSVLTVLHQWDLNGKEYKCKVSNKALPAIETK 262

Qy 121 ISKAVQPRERPVQVYLPPSRDELTKQNSITLUVKGFSVFLFPKPKOTLMISRTPEVCVVVDVSHDPEVK 180

Db 263 ISKAKQGQPREPVQVYLPPSRBMETKQNSITLCLVKGFSVFLFPKPKOTLMISRTPEVCVVVDVSHDPEVK 322

Qy 181 PVLDVGSGFPLYSKLTVDKSRQWQGQNVFGSVMHEALHNHQQLSLSRGK 232

Db 323 PVLDGSFFPLYSKLTVDKSRQWQGQNVFGSVMHEALHNHQQLSLSRGK 374

RESIDUE 3

S31866

19 gamma-1 chain C region - synthetic

C; Species: synthetic

A; Note: Homo Sapiens (man) gene engineered and expressed in Escherichia coli

C; Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000

R; Filipula, D.

submitted to the EMBL Data library, February 1993

A; Description: Screening method for protein-protein interactions of cloned gene products.

A; Reference number: S31866

A; Accession: S31866

A; Molecule type: mRNA

A; Residues: 1-255 <FILE>

A; Cross-references: EMBL:X70421; NID:933068; PIDN:CAA49866.1; PID:933069

C; Keywords: immunoglobulin

F; 1-22/Region: Bacteriophaga coli outer membrane protein A precursor

F; 23-255/Region: human Ig gamma-1 chain C region

Query Match 96.6%; Score 1217; DB 4; Length 255;

Best Local Similarity 96.6%; Pred. No. 1e-84; 5; Mismatches 0; Indels 0; Gaps 0;

Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 2

S6339

Ig heavy chain V region precursor - human

C; Species: Homo Sapiens (man)

C; Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

C; Accession: S69339; S77664

R; Khamlichchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Bio. J. Biochem. 229, 54-60, 1995

**RESULT 4**

Ig gamma chain C region - chimpanzee  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C;Accession: PT0207  
R;Burkhardt, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A;Title: Nucleotide sequence of chimpanzee IgC and hinge regions.  
A;Reference number: PT0207; MUID:91287716; PMID:2062315

A;Molecule type: mRNA  
A;Residues: 1-234 <EHR>  
C;Superfamily: immunoglobulin homology <IMM>  
F;48-117/Domain: immunoglobulin homology

Query Match 93.0%; Score 117; DB 2; Length 234;  
Best Local Similarity 95.6%; Pred. No. 2.3e-81; Mismatches 4; Indels 0; Gaps 0;  
Matches 215; Conservative 6; MisMatches 6; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 60  
Db 10 EPKSCDTTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 69

Qy 61 NWYDGVEVINKTKPREEQYNSTRVWSVLTIVLQHNWMGKEYKCKVSNSKALPPIKT 120  
Db 70 NWYDGVEVINKTKPREEQYNSTRVWSVLTIVLQHNWMGKEYKCKVSNSKALPPIKT 129

Qy 121 ISKAQVQPRQQVYTLPPSDDELTKNQVSITCLVKGFPYPSDIAVEWESNOOPENNYKTP 180  
Db 130 ISKAQVQPRQQVYTLPPSDDELTKNQVSITCLVKGFPYPSDIAVEWESNOOPENNYKTP 189

Qy 181 PVLDVGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQQRS 225  
Db 190 PVLDGSFPLYSKLTVDSRQGNVFSCSVMHEALTHNHYTQKS 234

**RESULT 5**

A23511 Ig gamma-3 chain C region (haplotype G3m(b)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C;Accession: A23511  
R;Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: ccc  
A;Reference number: A23511; MUID:86148507; PMID:3081877  
A;Accession: A23511  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056

Qy 1 EPKSCDKTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 60  
Db 146 EPKSCDTTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 205

Qy 61 NWYDGVEVINKTKPREEQYNSTRVWSVLTIVLQHNWMGKEYKCKVSNSKALPPIKT 120  
Db 206 KNYDGVEVINKTKPREEQYNSTRVWSVLTIVLQHNWMGKEYKCKVSNSKALPPIKT 265

Qy 121 ISKAQVQPRQQVYTLPPSDDELTKNQVSITCLVKGFPYPSDIAVEWESNOOPENNYKTP 180  
Db 266 ISKAQVQPRQQVYTLPPSDDELTKNQVSITCLVKGFPYPSDIAVEWESNOOPENNYKTP 235

Qy 181 PVLDVGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQRSLSLSPGK 232  
Db 326 PVLDGSFPLYSKLTVDSRQGNVFSCSVMHEALTHNHYTQSLSLSPGK 377

**RESULT 6**

A60764 Ig gamma-3 chain C region, form LAT - human  
C;Species: Homo sapiens (man)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C;Accession: A60764  
R;Huck, S.; Lestranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A;Reference number: A60764; MUID:9007613; PMID:571587

A;Accession: A60764  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPROT:OBNA4Y9  
C;Superfamily: immunoglobulin homology <IMM>  
F;20-85/Domain: immunoglobulin

Query Match 90.2%; Score 1136; DB 2; Length 377;  
Best Local Similarity 89.7%; Pred. No. 2.1e-78; Mismatches 11; Indels 13; Gaps 0; Gaps 0;  
Matches 208; Conservative 11; MisMatches 13; Indels 13; Gaps 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 60  
Db 146 EPKSCDTTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 205

Qy 61 NWYDGVEVINKTKPREEQYNSTRVWSVLTIVLQHNWMGKEYKCKVSNSKALPPIKT 120  
Db 206 KNYDGVEVINKTKPREEQYNSTRVWSVLTIVLQHNWMGKEYKCKVSNSKALPPIKT 265

Qy 121 ISKAQVQPRQQVYTLPPSDDELTKNQVSITCLVKGFPYPSDIAVEWESNOOPENNYKTP 180  
Db 266 ISKAQVQPRQQVYTLPPSDDELTKNQVSITCLVKGFPYPSDIAVEWESNOOPENNYKTP 325

Qy 181 PVLDVGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQRSLSLSPGK 232  
Db 326 PVLDGSFPLYSKLTVDSRQGNVFSCSVMHEALTHNHYTQSLSLSPGK 377

**RESULT 7**

G3HNU1 Ig gamma-3 heavy chain disease protein - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1979 #sequence\_revision 23-Oct-1991 #text\_change 16-Jul-1999  
C;Accession: A04042; A92219; A9018; A39195; A02149  
R;Frangione, B.; Rosenwasser, L.; Prelli, F.; Franklin, E.C.  
Biochemistry 19, 4304-4308, 1980  
A;Title: Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma3 heavy-  
C;Keywords: immunoglobulin  
C;Contents: heavy chain disease protein Wis  
A;Accession: A04042  
A;Molecule type: protein  
A;Residues: 1-289 <FR>  
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co-  
A;Note: the sequence of residues 42-76 was taken from the reference that follows  
R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.  
J. Biol. Chem. 252, 883-889, 1977.

Qy 1 EPKSCDKTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 60  
Db 146 EPKSCDTTHTCPPCPAPELGGPSVLFLPPPKPDKTMISRPTPEVTCVWVDSHEDPEVKF 205

A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
A;Reference number: A92219; MUID:77118561; PMID:402363  
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein w  
A;Accession: A92219  
A;Molecule type: protein  
A;Residues: 12-97 <MIC>  
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
A;Contents: heavy chain disease protein zuc, partial sequence corresponding to residues  
A;Molecule type: protein  
A;Residues: 59-125; 'EB', 128-226, 228-289 <WOL>  
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
R;Alexander, R.; Steinmetz, M.; Barrault, D.; Frangione, B.; Franklin, B.C.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A., 79, 3260-3264, 1982  
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion  
A;Reference number: A93915; MUID:8224835; PMID:6808505  
A;Contents: heavy chain disease protein Omm  
A;Accession: A93915  
A;Molecule type: RNA  
A;Residues: 12-70-72-114-116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
A;Note: a carboxy-terminal Lys is removed post-translationally  
A;Note: this sequence may represent an allelic form or another gamma chain subclass  
C;Comment: The heavy chain disease protein Wis is shown.  
C;Genetics:  
A;Gene: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 1q32.33-1q43.2-3.3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid  
F;203-210/Domain: immunoglobulin homology <IM>  
F;1/Modif site: pyrrolidine carbonylic acid (Gln) #status experimental  
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 89.1%; Score 1123; DB 1; Length 289;  
Best Local Similarity 88.3%; Pred. No. 1.5e-77; Mismatches 14; Indels 0; Gaps 0;  
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPPCPAPELIGGSPVFLFPKPDKTLMISRPTPEVTCVVVDVSHDPEVKF 60  
Db 59 EPKSCDKTHTCPPCPAPELIGGSPVFLFPKPDKTLMISRPTPEVTCVVVDVSHDPEVQF 118  
QY 61 NWYTDGVETVHKVKTPRESYNTVVSFLTVLQVNWNGKEYKKVSKNKLAPIKT 120  
Db 119 KWWYDGVOVNEAKTKPREQQFNSTFRVSVLTVLHQNLWIDKEYKCKVSNKLAPEKT 178  
QY 121 ISKAKVQPRPQQVYLPLPSDELTNQSVLTCIJKGFYPSDIAVEWESNGOPENNYKTP 180  
Db 179 ISKAKVQPRPQQVYLPLPSBEMTNQSVLTCIJKGFYPSDIAVEWESNGOPENNYKTP 238  
QY 181 PVLDGSVGSFLYLYSKLTIVDKSRWQOQNVFSCSVMHMLAHNNYQQSLSLSPG 231  
Db 239 PMLUDSGSFLYLYSKLTIVDKSRWQOQNVFSCSVMHMLAHNNYQQSLSLSPG 289  
RESULT 8  
GRU Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Accession: 30-Apr-1981 #sequence revision 13-Jun-1993 #text\_change 09-Jul-2004  
R;Ellison, J.; Hood, L. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>

A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CA858438.1; PI  
A;Note: Lys-226 is probably removed posttranslationally  
R;Wang, A.C.; Tung, J.; Rudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fu  
A;Reference number: A92809; MUID:81007873; PMID:5774012  
A;Contents: myeloma protein Til  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19, Q, 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 738-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a l  
A;Reference number: A90525; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85-132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g6  
A;Reference number: A93132; MUID:8011419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOE>  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A93591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A9053; MUID:72035050; PMID:4940072  
A;Contents: annotation; myeloma protein Sa; disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:6906124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 1q32.33-1q43.2-3.3  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM>  
F;113-202/Domain: immunoglobulin homology <IM2>  
F;219-305/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;21-83,140-200,246-304/Disulfide bonds: #status experimental  
F;101,105/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;112,106/Disulfide bonds: interchain (covalent) #status predicted  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.9%; Score 1107; DB 1; Length 326;  
Best Local Similarity 88.4%; Pred. No. 2.8e-76; Mismatches 11; Indels 4; Gaps 2;  
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;  
QY 1 EPKSCDKTHTCPPCPAPELIGGSPVFLFPKPDKTLMISRPTPEVTCVVVDVSHDPEVKF 60  
Db 99 ERKCVVE--CPREAPP-WAGSPVFLFPKPDKTLMISRPTPEVTCVVVDVSHDPEVQF 154  
QY 61 NWYTDGVETVHKVKTPRESYNTVVSFLTVLQVNWNGKEYKKVSKNKLAPIKT 120  
Db 155 NWYTDGVETVHKVKTPREQQFNSTFRVSVLTVLHQNLWIDKEYKCKVSNKLAPEKT 214  
QY 121 ISKAKVQPRPQQVYLPLPSDELTNQSVLTCIJKGFYPSDIAVEWESNGOPENNYKTP 180

**RESULT 9**

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Accession: A90933; A0249; A02150

R;Elliason, J.; Bubbaum, J.; Hood, L.

DNA 1..11-18..1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933; Molecule type: DNA

A;Residues: 1-327 <ELL>

A;Cross-references: UNIPROT:P01861

A;Note: the sequences was determined from the germline gene

R;Pink, J.R.L.; Batterly, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A;Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant region

A;Reference number: A90249; MUID:70207560; PMID:4192699

A;Accession: A90249

A;Molecule type: Protein

A;Residues: 1-30..81-326 <PIN>

C;Genetics:

A;Gene: GDB:ICHG4

A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes: immunoglobulin C region; immunoglobulin homology

C;Superfamily: immunoglobulin

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

A;Intron: 99/1..111/1; 221..1

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>

F;240-240/Domain: immunoglobulin homology <IM3>

F;14-Disulfide bonds: interchain (to light chain) #status experimental

F;27-83..141-201..247-305/Disulfide bonds: #status predicted

F;106-109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.1% Score 1097; DB 1; Length 327; Best Local Similarity 90.5%; Pred. No. 1..6e-75; Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 11 CPPCAPPAPLLGGPSVPLFPKPKPDKLMSRTPETCVWVDVSHDEPEVKENWYDGVEVH 70

Db 106 CPSCPAPEFTGGPSVFLFPKPKPDKLMSRTPETCVWVDVSHDEPEVKENWYDGVEVH 165

Qy 71 NVKTKPREEQNSTYRVSVTIVLHQHNWNGKEYKCKVSKNALKAPIEKTKSKVQPRE 130

Db 166 NAKTKPREEQNSTYRVSVTIVLHQHDWINGKEYKCKVSKNKGKPSIEKTIKSKQGPRE 225

Qy 131 PQVWYLPSPSDELTINQVSLTCVKGKFYPSDIAVEWESQOPENNYKTPPVLSVGSEF 190

Db 226 PQQVYLPSSQBMKQVSLLTCVKGKFYPSDIAVEWESQOPENNYKTPPVLSVGSEF 285

Qy 191 LYSLKLTVDKSRWQGNVFSVCSVMHEALHNHYQKSLSLSLGK 232

Db 286 LYSRITVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSLGK 327

RESULT 10

GHRB Ig gamma chain C region - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

Qy 225 SLSLSPGK 232

Db 316 SISRSRGK 323

C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004

C;Accession: K91779; A00290; A93928; A90245; A94416; A02161

R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18..387-397, 1983

A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotypic allele

A;Reference number: A91749; MUID:8400930; PMID:6313520

A;Accession: A91749

A;Molecule type: mRNA

A;Residues: 1-323 <BER>

A;Cross-references: UNIPROT:P01870

A;Note: this sequence has the d12 allotypic marker, 104-thr, and the e14 marker, 185-thr

R;Martens, C.L.; Moore, K.W.; Steinmeier, M.; Hood, L.; Knight, K.L.

Biochem. J. 151, 337-349, 1975

A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulins

A;Reference number: A90290; MUID:76135469; PMID:1243651

A;Accession: A90290

A;Molecule type: protein

A;Residues: 1-47, 'B', 49-71, 'PV', 72-128 <PR>

R;Martens, C.L.; Moore, K.W.; Steinmeier, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A;Title: Heavy chain genes of rabbit IgG; Isolation of a cDNA encoding gamma heavy chain

A;Reference number: A93928; MUID:83299917; PMID:6193512

A;Accession: A93928

A;Molecule type: mRNA

A;Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>

A;Cross-references: GB:ML6426; NID:G16511; PID:AA31289\_1; PID:G165112

A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker

R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C

A;Reference number: A90245; MUID:70110015; PMID:5461106

A;Accession: A90245

A;Molecule type: protein

A;Residues: 132-143, 'B', 145-161 <PRU>

R;Hill, R.L.; Lebowitz, H.E.; Pellow Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp 109-127, Almqvist and Wiksell,

A;Reference number: A94416

A;Accession: A94416

A;Molecule type: protein

A;Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'B', 219-232, 'Q', ;

A;Note: this has the e15 allotypic marker, 185-Ala

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes: immunoglobulin C region; immunoglobulin homology

C;Superfamily: immunoglobulin

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;21-82/Domain: immunoglobulin homology <IM1>

F;130-139/Domain: immunoglobulin homology <IM2>

F;236-303/Domain: immunoglobulin homology <IM3>

F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.1% Score 883; DB 1; Length 323; Best Local Similarity 64.5%; Pred. No. 2..2e-59; Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

Qy 1 EPKSKCDKTH-----TC--PPCPAPAPLLGGPSVFLPPKPKPDKLMSRTPEV 44

Db 76 QPVTCVVAHATNTKDKVTWAPSTCCKPTCPCPPLGLGGPSVFLPPKPKPDKLMSRTPEV 135

Qy 45 TCWVWDVSHDEPEVKENWYDGVEVHNVKTPREQSYNSTYRVSVLTVLHQHNWNGKEY 104

Db 136 TCVWVWDVSDPDEPEVKENWYDGVEVHNVKTPREQSYNSTYRVSVLTVLHQHNWNGKEY 195

Qy 105 KCKVSKNALKAPIEKTKSKVQPREQSYNSTYRVSVLTVLHQHNWNGKEYKTPPVLSVGSEF 164

Db 196 KCKVSKNALKAPIEKTKSKVQPREQSYNSTYRVSVLTVLHQHNWNGKEYKTPPVLSVGSEF 255

Qy 165 EWESQOPENNYKTPPVLSVGSEFYLGSVFLYPSVLSRQDNVFCSVMEALHNHYQ 224

Db 256 EWEKQKAENYKTPAVLSDGSFVFLYNKLSVPTSEWQGDVFCSVMEALHNHYQ 315



Biochemistry 10, 9-17, 1971  
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami  
A;Reference number: A90359; MUID:7105486; PMID:5538616  
A;Accession: A90359  
A;Molecule type: protein  
A;Residues: 69-133:312-329 <TR>  
R;Tracey, D.E.; Cobra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A;Reference number: A90384; MUID:75036072; PMID:4429665  
A;Molecule type: protein  
A;Residues: 134-225 <TR>  
R;Trischmann, T.M.; Cobra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A;Reference number: A90385; MUID:75036073; PMID:4609467  
A;Accession: A90385  
A;Molecule type: protein  
A;Residues: 227-311 <TR>  
R;Olivera, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A;Title: Interchain disulfide bridges of guinea pig gamma-2 immunoglobulin.  
A;Reference number: A9054; MUID:71058474; PMID:4922544  
A;Contents: annotation; disulfide bonds  
A;Note: Cys-16 is involved in a heavy-light chain bond  
A;Note: Cys-105...Cys-107, and Cys-110 form inter-heavy chain bonds  
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κα)  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κα)  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;21-81:Domain: immunoglobulin homology <IM1>  
F;135-204:Domain: immunoglobulin homology <IM2>  
F;241-310:Domain: immunoglobulin homology <IM3>  
F;28-79:Disulfide bonds: #status experimental  
F;142-202:Disulfide bonds: #status experimental  
F;178:Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;248-308:Disulfide bonds: #status experimental

Query Match 68 1%; Score 858; DB 1; Length 329;  
Best local Similarity 67.4%; Pred. No. 1.7e-57;  
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

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Qy 1 EPKSCDKTKTHCPPCPAPELLGPGSPVFLPPPKPDLMISRPTPEVTCVVVDVSHEDPEYKFNNYDGVE 60
Db 101 ZPBPC---TCPKCPPENLGGPSVIFPPKPKDTLMISLTPRVTCVVVDVSDPEVQF 156

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Qy 61 NWYDQEVEHVKTKPKEQQNTRIVSIVLVLQHNMWNGKEYCKVSKKALPPIEKT 120
Db 157 TWFDVNPKVPGNAETKPRVEQNTTFRVSVLPQIHOQDWLRKEFKCKVYKNAKALPPIEKT 216

Qy 121 ISKAKVQPREROVYTIPPSRDLTQVNLQVSLLTCLVKCFYPSDIAVWESENQGP- ENNYKT 178
Db 217 ISKTKGAAPRDPVYRTPSRDLSKSKVSYTCLILINFFPADIHEVWASNRVPVSKERYN 276

Qy 179 TPPVLDGSVGSFPLYSKLTVDKSRWQGNVFSCSVMHEALRHMYQORSLSLSPG 231
Db 277 TPPIEDADGSYFLYSLKLTVDKSAWDGTVYICSVMHEALRHMYTOKAISRSPG 329

A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03778; NID:9433121; PID:AA52216.1; PID:9433122  
C;Genetics:  
A;Gene: IgG1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;133-202:Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 847.5; DB 2; Length 328;  
Best Local Similarity 69.3%; Pred. No. 1.1e-56;  
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;  

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Qy 10 TCPCCPAELLGGSVFLPPPKPDLMISRPTPEVTCVVVDVSHEDPEYKFNNYDGVE 69
Db 105 TCPICPGCE-VAGPSVIEFPKPKDTLMISLTPEVTCVVVDVSKHAEVQFWSWYDGVE 163

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Qy 70 HNVKTKPREQYNSTRVISLVTULHQHNWNGKEYCKVSKNSKALPAPIEKTISKAVQPR 129
Db 164 HTAEITRKPKEDQFNSTYRVISVLPQHODWIKGKEFKCKVSKNSKALPAPIEKTISKAVQPR 223

Qy 130 EPQVTLPPRSDELTRNQVSLTCLVKGFYPSDIAVEWESNGO- PENNYKTTTPVLDVSG 187
Db 224 BPQVITLPPPABELSRSKVKITLCLVIGFIPPDIHIVEWSKGQGPBPENTTRITPQQDVG 283

Qy 188 SFEVYSLKLTDSRQGNWFCSTUNHEALRHMYQORSLSLSPG 232
Db 284 TPFYLSKLAVDKARNDHGDKPKECAVNHEALRHMYQKSRTQK 328

Search completed: June 7, 2005, 09:02:35

Job time : 26.4421 secs

RESULT 15

I47158  
IG gamma 1 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Sequence: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47158  
J; Immunol. 153:3365-3373, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
A;Accession: I47158  
A;Status: preliminary; translated from GB/EMBL/DDBJ

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 08:39:41 ; Search time 114.197 Seconds

(without alignments)

1040.329 Million cell updates/sec

Title: Perfect score: US-10-000-439-3

Sequence: EFKSCDTHTCPPCPAPELL.....MEBALINHMQQTSLSISPGK 232

Scoring table: BroSUM62

Searched: GapOp 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

\* Query Match length DB ID Description

1 1225 97.2 330 1 GCL HUMAN P01857 homo sapien

2 1225 97.2 465 2 Q6GMX6 homo sapien

3 1225 97.2 466 2 Q6In178 homo sapien

4 1225 97.2 469 2 Q7ZTP5 homo sapien

5 1225 97.2 470 2 Q6PJA4 homo sapien

6 1225 97.2 470 2 Q7Z5W1 homo sapien

7 1225 97.2 472 2 Q6N089 homo sapien

8 1225 97.2 475 2 Q6Gmw7 homo sapien

9 1225 97.2 476 2 Q6Gmx1 homo sapien

10 1225 97.2 679 2 Q96PQB homo sapien

11 1221 96.9 473 2 Q6P055 homo sapien

12 1221 96.9 474 2 Q6Mzq6 homo sapien

13 1221 96.9 480 2 Q6N094 homo sapien

14 1221 96.9 481 2 Q6N097 homo sapien

15 1221 96.9 482 2 Q7Z351 homo sapien

16 1219 96.7 348 2 Q6PYKL homo sapien

17 1219 96.7 473 2 Q6MV77 homo sapien

18 1219 96.7 478 2 Q6P181 homo sapien

19 1219 96.7 480 2 Q6PJF1 homo sapien

20 1218 96.7 466 2 Q6N096 homo sapien

21 1214 96.3 475 2 Q6N095 homo sapien

22 1214 96.3 544 2 Q6PJ5 homo sapien

23 1196 94.9 487 2 Q65ZL2 muS sp. fv/

24 1138 90.3 354 2 Q86tt2 homo sapien

25 1138 90.3 518 2 Q6N030 homo sapien

26 1134 90.0 521 2 Q8n4Y9 homo sapien

27 1128 89.5 290 2 Q01860 homo sapien

28 1123 89.1 509 2 Q8nf17 homo sapien

29 1107 87.9 326 1 Q6C2 HUMAN

30 1107 87.9 417 2 Q01859 homo sapien

31 1104 87.6 464 2 Q6mzu6 homo sapien

RESULT 1.

ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	Q01857;			
DT	21-JUL-1985 (Rel. 01, Last sequence update)			
DT	25-OCT-2003 (Rel. 45, last annotation update)			
DR	Ig gamma-1 chain C region.			
GN	Name=IGHG1			
OS	Homo sapiens (Human)			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RA	Cunningham B.A., Rutishauser U., Gaill W.E., Gottlieb P.D.,			
RA	Edelman M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RL	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=7707269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chromatographic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";			
RT	RJ. Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).			
RT	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=81289131; PubMed=688494;			
RA	Schmidt W.R., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			

RA	Gall W.E.; Edelman G.M.;	FT DOMAIN 111	223	CH2.
RT	"The covalent structure of a human gamma G-immunoglobulin. X.	FT DOMAIN 224	330	CH3.
RT	Inttrachain disulfide bonds."	FT DISULFID 27	83	Interchain (with light chain).
RL	Biochemistry 9:3188-3196(1970).	FT DISULFID 103	103	Interchain (with heavy chain).
RN	[7]	FT DISULFID 109	109	Interchain (with heavy chain).
RP	DISULFIDE BONDS.	FT DISULFID 112	112	
RX	MEDLINE=7707267; PubMed=1002129;	FT DISULFID 144	204	
RA	Dreicer L.; Schwarz J.; Reichel W.; Hilschmann N.;	FT DISULFID 250	308	N-linked (GlcNAc, -)-.
RT	"Role of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges";	FT CARBOHYD 180	180	K->R (in GlcM(3) marker).
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).	FT VARIANT 97	97	/FTid=VAR_003886. D->E (in GlcM(non-1) marker).
RN	[8]	FT VARIANT 239	239	/FTid=VAR_003887. L->M (in GlcM(non-1) marker).
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).	FT VARIANT 241	241	/FTid=VAR_003888.
RX	MEOLINEB81200100; PubMed=7236608;	FT VARIANT 241	241	
RA	"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus 2.9- and 2.8-A resolution.";	FT STRAND 23	24	
RL	Biochemistry 20:2361-2370(1981).	FT STRAND 26	33	
CC	-1- MISCELLANEOUS: Nie has the GlcM(17) allotypic marker, 97-K, and the GlcM(1) markers, 231-D and 241-L. KOL and EU sequences have the GlcM(3) marker and the GlcM (non-1) markers.	FT STRAND 50	52	
CC	-1- MISCELLANEOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.	FT STRAND 57	58	
CC	-1- MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272.	FT TURN 59	61	
CC	-1- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.	FT STRAND 62	71	
CC		FT HELIX 73	75	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	FT TURN 76	78	
CC		FT STRAND 82	87	
CC		FT TURN 88	91	
CC		FT STRAND 92	97	
CC		FT TURN 102	103	
CC		FT STRAND 122	126	
CC		FT HELIX 130	134	
CC		FT TURN 136	137	
CC		FT STRAND 141	149	
CC		FT STRAND 157	162	
CC		FT TURN 163	164	
CC		FT STRAND 165	167	
CC		FT STRAND 171	172	
CC		FT TURN 176	177	
CC		FT STRAND 179	180	
CC		FT STRAND 183	190	
DR	PTR: A93433; GHHU	FT HELIX 193	197	
DR	PDB: 1A07; X-ray; H=1-103.	FT TURN 198	199	
DR	PDB: 1D5B; X-ray; H=1-101.	FT STRAND 202	207	
DR	PDB: 1D6V; X-ray; H=1-101.	FT TURN 209	210	
DR	PDB: 1D8V; X-ray; H=1-120-326.	FT STRAND 215	219	
DR	PDB: 1EAK; X-ray; A/B=05-329.	FT STRAND 227	227	
DR	PDB: 1FC1; X-ray; A/B=06-329.	FT STRAND 230	234	
DR	PDB: 1FC2; X-ray; D=105-329.	FT HELIX 238	242	
DR	PDB: 1FC2; X-ray; A=121-326.	FT STRAND 245	256	
DR	PDB: 1H2H; X-ray; H/K=1-130.	FT STRAND 261	266	
DR	PDB: 1I7Z; X-ray; B/D=1-103.	FT TURN 267	268	
DR	PDB: 1IT5; X-ray; A/B=107-330.	FT STRAND 269	270	
DR	PDB: 1IXX; X-ray; A/B=107-330.	FT HELIX 274	276	
DR	PDB: 1L6X; X-ray; A=120-326.	FT STRAND 280	281	
DR	PDB: 1O0X; X-ray; A/B=19-330.	FT TURN 283	284	
DR	PDB: 2RGS; X-ray; H=1-103.	FT STRAND 287	296	
DR	PDB: 3GNC; X-ray; H=1-103.	FT HELIX 297	301	
DR	MTM: 1A7100; -	FT TURN 302	303	
DR	GO: GO:000564; C-membrane fraction; NAS.	FT STRAND 306	311	
DR	GO: GO:0003833; F-antigen binding; TAS.	FT TURN 313	314	
DR	GO: GO:0006955; P-immune response; NAS.	FT HELIX 316	318	
DR	InterPro: IPR003006; Ig_MHC.	FT STRAND 319	324	
DR	PFam: PF00047; Ig; 3.	FT SEQUENCE 330 AA;	36106 MN;	3770EB106C2FA33D CRC64;
DR	PROSITE: PS00383; Ig_LIKE; 3.			
KW	3D-structure; Direct_protein_sequencing; Glycoprotein;	Query Match 97.2%; Score 1225; DB 1; Length 330;		
KW	Immunoglobulin_C_region; Immunoglobulin_domain.	Best local Similarity 97.0%; Pred. No. 1; Be-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
FT	NON_TER 1	Qy 1 EPKSCDKTHTPCPAPALELGGPSVFLFRPKPKDTLMTSRTPETVCVVVDVSHDPEVK 60		
FT	DOMAIN 1	FT 99 EPKSCDKTHTPCPAPALELGGPSVFLFRPKPKDTLMTSRTPETVCVVVDVSHDPEVK 158		
FT	DOMAIN 99			
FT	DOMAIN 110			
FT	Hinge.			



DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.	DR	PROSITE; PS050835; IG_LIKE; 4.
SQ	SEQUENCE 466 AA; 5053 MW; 53EB0BCEDE81076E CRC64;	SQ	SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAP795C CRC64;
Query Match	Best local Similarity 97.2%; Score 1225; DB 2; Length 466; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	Query Match	Best local Similarity 97.2%; Score 1225; DB 2; Length 469; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Db	EPKSCKDTKTCPPAPELGGPSVFLPPPKPDKTLMISRTPETCVWVDVSHDPEVKF 60	Db	EPKSCKDTKTCPPAPELGGPSVFLPPPKPDKTLMISRTPETCVWVDVSHDPEVKF 60
Qy	1 EPKSCKDTKTCPPAPELGGPSVFLPPPKPDKTLMISRTPETCVWVDVSHDPEVKF 60	Qy	1 EPKSCKDTKTCPPAPELGGPSVFLPPPKPDKTLMISRTPETCVWVDVSHDPEVKF 60
Db	EPKSCKDTKTCPPAPELGGPSVFLPPPKPDKTLMISRTPETCVWVDVSHDPEVKF 294	Db	EPKSCKDTKTCPPAPELGGPSVFLPPPKPDKTLMISRTPETCVWVDVSHDPEVKF 294
Qy	61 NWYDGVEHNVKTKPREEQYNSTYRVWSLTIVLHQNMNGKEKCKVSNKALPPIKT 120	Qy	61 NWYDGVEHNVKTKPREEQYNSTYRVWSLTIVLHQNMNGKEKCKVSNKALPPIKT 120
Db	295 NWYDGVEHNVKTKPREEQYNSTYRVWSLTIVLHQNMNGKEKCKVSNKALPPIKT 354	Db	295 NWYDGVEHNVKTKPREEQYNSTYRVWSLTIVLHQNMNGKEKCKVSNKALPPIKT 354
Qy	121 ISKAKVQPRPVQVTLLPSRDELTKNOVSITCLVKGFYPSDIAVEWESENQOPENNYKTP 180	Qy	121 ISKAKVQPRPVQVTLLPSRDELTKNOVSITCLVKGFYPSDIAVEWESENQOPENNYKTP 180
Db	355 ISKAKGQPRBPQVTVLPPSRDELTKNOVSITCLVKGFYPSDIAVEWESENQOPENNYKTP 414	Db	355 ISKAKGQPRBPQVTVLPPSRDELTKNOVSITCLVKGFYPSDIAVEWESENQOPENNYKTP 414
Qy	181 PVLDVGSGSPFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQOQLSLSPGK 232	Qy	181 PVLDVGSGSPFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQOQLSLSPGK 232
Db	415 PVLDGSGSPFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQOQLSLSPGK 466	Db	418 PVLDGSGSPFLYSKLTVDKSRWQGNVFSCSVMHEALTHNHYQOQLSLSPGK 466
<b>RESULT 4</b>			
Q727PS	PRELIMINARY; PRT; 469 AA.	Q727PS	PRELIMINARY; PRT; 469 AA.
AC	Q727P5; 01-OCT-2003 (TREMBLER. 25, Created)	AC	Q727P5; 01-OCT-2003 (TREMBLER. 25, Last sequence update)
DT	01-OCT-2003 (TREMBLER. 25, Last sequence update)	DT	01-MAR-2004 (TREMBLER. 26, Last annotation update)
DB	IGIG1 protein.	DB	IGIG1 protein.
OS	Homo sapiens ('Human').	OS	Homo sapiens ('Human').
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	TISSUE=Spleen; MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Q727P5; Feingold E.A., Grouse L.H., Derge J.G., Klaunser R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Robin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhall S.J., Rodriguez S., Grimes J.W., Green E.D., Dickson M.C., Rodriguez S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutiffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez S., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RC	TISSUE=Primary B-Cells; MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Q727P5; Feingold E.A., Grouse L.H., Derge J.G., Klaunser R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhall S.J., Rodriguez S., Grimes J.W., Green E.D., Dickson M.C., Rodriguez S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutiffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez S., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	Strausberg R.; Submitted (APP-2003) to the EMBL/GenBank/DBJ databases.	RC	Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC051328; AAH51328.1; -.	RL	EMBL; BC018747; AAH18747.1; -.
DR	HSSP; P01857; IIZRH.	DR	HSSP; P01861; IADQI.
InterPro	IPR007110; Ig-like.	InterPro	IPR003599; Ig cl.
DR	InterPro; IPR003597; Ig cl.	DR	InterPro; IPR007110; Ig-like.
InterPro	IPR003066; Ig_MHC.	InterPro	IPR003591; Ig cl.
DR	InterPro; IPR003596; Ig v.	DR	InterPro; IPR003066; Ig_MHC.
Pfam	PF07654; Cl-set; 3.	InterPro; IPR003596; Ig_v.	InterPro; IPR003596; Ig_v.
SMART	SM00406; Ig v; 1.	SMART	SM00406; Ig v; 1.

DR	Pfam; PF07654; Cl-set; 3.
DR	SMART; SMO0409; IG; 2.
DR	SMART; SMO0407; IGC1; 3.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PS00825; IG_LIKE; 4.
DR	PROSITE; PS00201; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
SQ	SEQUENCE 470 AA; 51715 MW; 7B4556A11FD7D9 CRC64;
Query Match	97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity	97.0%; Pred. No. 2.8e-88;
Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
AC	1 EPKSCDKHTCPCCPAPBLGGPSVFLPPKPKDTLMISRTPETVCVVVDVSHEDPEVKP 60
DT	01-OCT-2003 (TREMBrel. 25, Last sequence update)
DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
RN	[1] SEQUENCE FROM N.A.
RC	TISSUE=Spleen; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242038999;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschuler R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altshul S.F., Zeeberg B., Bustein R., Diatchenko L., Marusina K., Farmer A.B., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brown S.S., Lockettano N.A., Peters K.G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan J.J., Malek J.A., Guarante P.H., Richards S., Warley K.C., Hall S., Garcia A.M., Gay L.J., Hulyk S.W., Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J., Makrilia M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]
RN	SEQUENCE FROM N.A.
RC	TISSUE=Spleen; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC053984; AAH55984.1; -. HSSP; P01857; IHZH.
DR	InterPro; IPR003597; Ig_c1.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; Cl-set; 3.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PS00201; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
SQ	SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match	97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity	97.0%; Pred. No. 2.8e-88;
Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
AC	1 EPKSCDKHTCPCCPAPBLGGPSVFLPPKPKDTLMISRTPETVCVVVDVSHEDPEVKP 60
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)
DE	Hypothetical protein DKFZp686P15220; Name=DKFZp686P15220;
GN	Homo sapiens (Human);
OS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
RN	[1] SEQUENCE FROM N.A.
RC	TISSUE-Human rectum tumor; The German Human CDNA Consortium; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RA	Wanbutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Roho G., Han M., Wienmann S.; EMBL; BX640527; CAA45781.1; -. DR InterPro; IPR0161; IANQ. DR InterPro; IPR003599; Ig. DR InterPro; IPR007110; Ig-like. DR InterPro; IPR003597; Ig_c1. DR InterPro; IPR003006; Ig_MHC. DR InterPro; IPR003596; Ig_v. DR Pfam; PF07654; Cl-set; 3. DR SMART; SMO0409; Ig; 2. DR SMART; SMO0407; IGC1; 3. DR SMART; SMO0406; IGV; 1. DR PROSITE; PS00835; IG_LIKE; 4. DR PROSITE; PS00201; IG_MHC; UNKNOWN_2.
RN	SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
Query Match	97.2%; Score 1225; DB 2; Length 472;
Best Local Similarity	97.0%; Pred. No. 2.8e-88;
Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
AC	1 EPKSCDKHTCPCCPAPBLGGPSVFLPPKPKDTLMISRTPETVCVVVDVSHEDPEVKP 60

Query	Match	97.2%	Score	1225	DB	2;	Length	475;
Best Local Similarity	97.0%	Pred.	No.	2, 86-88;				
Matches	225;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps
Db	1	EPKSCKTHTCPPCPAPAPELLGGSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	300					
Qy	121	ISKAKVQPREPVQVTLPSSRDELTKQVSJLCLVKQFYPSDIAVENESNGPENNKKTP	180					
Db	244	EPKSCKTHTCPPCPAPAPELLGGSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60					
Qy	61	NWYVGDGEVHNKTKPRBQYSNTSYRVSVTUVHQNMWNGKEYKCKVSNKALPAIETK	120					
Db	361	ISKAKGQPREPQVYTLPPSRDELTKQVSJLCLVKQFYPSDIAVENESNGPENNKKTP	420					
Qy	181	PVLDSVGSEFLYSKUTVDKSRWQGNVFSCSVVMHEALHNHYTQKSLSLSPKG	232					
Db	421	PVLDSGSPFLYSKUTVDKSRWQGNVFSCSVVMHEALHNHYTQKSLSLSPKG	472					
RESULT	8							
ID	OQGMW7	PRELIMINARY;	PRT;	475 AA.				
AC	OQGMW7;							
DT	05-JUL-2004	(TREMBREL. 27, Created)						
DR	05-JUL-2004	(TREMBREL. 27, Last sequence update)						
DE	Hypothetical protein.							
OC	Homo sapiens (Human).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX								
RN	NBBI_TaxID=9606;							
RP	[1]							
SEQUENCE FROM N.A.								
TISSUE-Spleen;								
RC	MDLINE#22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;							
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Cannici S., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Heitton B., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmwood J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]							
RC	RP	SEQUENCE FROM N.A.						
RC	TISSUE-Spleen;							
RC	Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.							
RC	DR	Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.						
RC	DR	InterPro: IPR003006; IG_C1.						
RC	DR	InterPro: IPR073782; AAH3773.1; -.						
RC	DR	InterPro: IPR003599; IG_v.						
RC	DR	InterPro: IPR007110; Ig-like.						
RC	DR	InterPro: IPR003597; Ig_C1.						
RC	DR	InterPro: IPR003006; Ig_MHC.						
RC	DR	InterPro: IPR003596; Ig_v.						
RC	DR	Pfam: PF007654; Cl-set; 3.						
RC	DR	Pfam: PF00047; ig; 4.						
RC	DR	SMART: SM00409; Ig; 2.						
RC	DR	SMART; SM00407; IgG1; 3.						
RC	DR	SMART; SM00406; IgV; 1.						
RC	DR	PROSITE; PS50835; Ig_LIKE; 4.						
RC	DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_2.						
RC	DR	Hypothetical protein.						
RC	DR	SEQUENCE 475 AA; 51997 MW; 2AEE55D736860FB CRC64;						

DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 476 AA; 52286 MW; 622AABASC62DDSD CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 476;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCPCPAPELLGGPSVLFPPKPKDTMISRTPETVCVVVDVSHEDPEVKF 60  
 Db 245 EPKSCDKTHCPCPAPELLGGPSVLFPPKPKDTMISRTPETVCVVVDVSHEDPEVKF 304

QY 61 NWYDGVEVHNVTKPREEQYNSTYRVSVLTLVHQNMKGKEYCKVSKNKLAPIKT 120  
 305 NWYDGVEVHNVAKTKEPQQYVLTQPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180

Db 121 ISAKYQPREPOVYTLLPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180

QY 365 ISAKQCPREPOVYTLLPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPENNYKTP 424

Db 181 PVLDVGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSISLSLSPK 232

QY 425 PVLDSDGSFLYSLKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSISLSLSPK 476

RESULT 10

ID 096P08 PRELIMINARY; PRT; 679 AA.  
 AC 096P08; 1 [1] (TrEMBLrel. 19, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Factor VII active site mutant immunoconjugate.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;

RA Hu Z., Garen A.; "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";  
 Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001). [2]

RP SEQUENCE FROM N.A.

RA Hu Z., Garen A.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF272774; AAC58686.2; -.

DR HSSP; P08709; IGLU.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005509; F:extracellular ion binding; IEA..

DR GO; GO:008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:tryptsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR00152; ASX\_hydroxyl\_S.

DR InterPro; IPR000742; EGFR\_C.

DR InterPro; IPR00181; EGFR\_Ca.

DR InterPro; IPR00620; EGFLike.

DR InterPro; IPR00710; Ig\_like.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR00306; Ig\_MIC.

DR InterPro; IPR001254; Peptidase\_S1.

DR InterPro; IPR00903; Pept\_Ser\_Cys.

DR InterPro; IPR00294; VitK\_dep\_Glu.

DR Pfam; PF07654; CL-set; 2.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00594; Glu; 1.

DR Pfam; PF00088; Trypsin; 1.

DR SMART; SM00179; EGF\_Ca; 1.

DR SMART; SM0069; GLA; 1.

DR SMART; SM00407; IgCl; 1.

DR SMART; SM0020; Tryp\_Spc; 1.

DR PROSITE; PS0010; ASY\_HYDROXYL; UNKNOWN\_1.

DR PROSITE; PS0022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS01186; EGF\_2; 1.

DR PROSITE; PS0026; EGF\_3; 1.

DR PROSITE; PS01187; EGF\_CA; 1.

DR PROSITE; PS00011; GLA\_1; 1.

DR PROSITE; PS5035; Ig\_LIKE; 2.

DR PROSITE; PS00230; IG\_MHC; UNKNOWN\_1.

DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KW EGF-like domain; Hydrolase; Protease; Serine protease.

SQ SEQUENCE 679 AA; 75552 MW; 0B0023A370A067A1 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 679;  
 Best Local Similarity 97.0%; Pred. No. 4.3e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCPCPAPELLGGPSVLFPPKPKDTMISRTPETVCVVVDVSHEDPEVKF 60  
 Db 448 EPKSCDKTHCPCPAPELLGGPSVLFPPKPKDTMISRTPETVCVVVDVSHEDPEVKF 507

QY 61 NWYDGVEVHNVAKTKEPQQYVLTQPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPENNYKTP 120

Db 568 ISAKYQPREPOVYTLLPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPENNYKTP 627

Db 508 NWYDGVEVHNVAKTKEPQQYVLTQPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGOPENNYKTP 567

QY 121 PVLDVGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSISLSLSPK 232

Db 628 PVLDSDGSFLYSLKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSISLSLSPK 679

RESULT 11

ID 06P055 PRELIMINARY; PRT; 473 AA.

RP SEQUENCE FROM N.A.

RP MEDLINE=212388257; PubMed=1247932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G., Klaunier R.D., Collins F.S., Wagner L., Sheinen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bielow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jorden H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marszina K., Farmer A.A., Rubin G.M., Hong D., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetze T.E., Brownstein M.J., Udin T.B., Tohuyoki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McElwain P.J., McKernan K.J., Malek J.A., Guarante P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzzey D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Tochman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Salska U., Smallall D.E., Schneich A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]





**This Page Blank (uspto)**

Run on:	June 7, 2005, 08:38:56 ; Search time 117.803 Seconds (without alignments)	OM protein - protein search, using sw model
Title:	US-10-000-439-3	Perfect score: 1660
Sequence:	1 EPKSCDKTHICPPCPAPEL.....MHEALHNHYQQRSLSLSPGK 232	Sequence: 1225 Human imm
Scoring table:	BLOSUM62	Score: 97.2
Searched:	Gapext 0.5	Score: 97.2
Total number of hits satisfying chosen parameters:	2105692	Minimum DB seq length: 0
Maximum DB seq length:	200000000	Maximum Match 0%
Post-processing:	Listing first 45 summaries	Maximum Match 100%
Database :	A. Geneseq_16Dec04;*	
	1: geneseqp1980s;*	
	2: geneseqp1990s;*	
	3: geneseqp2000s;*	
	4: geneseqp2001s;*	
	5: geneseqp2002s;*	
	6: geneseqp2003as;*	
	7: geneseqp2004as;*	
	8: geneseqp2004bs;*	
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
<b>SUMMARIES</b>		
Result No.	Score	Query Match Length DB ID Description
1	1260	100.0 232 6 AAO19665 Aao19665 Human IgG
2	1260	100.0 330 6 AAO19664 Aao19664 Human IgG
3	1260	100.0 569 6 AAO19668 Aao19668 Gb2 fusio
4	1225	97.2 232 2 AAW26232 Human IgG
5	1225	97.2 232 3 AAB28690 Human IgG
6	1225	97.2 232 4 AAB80897 Human IgG
7	1225	97.2 232 4 AAY2915 Human par
8	1225	97.2 232 5 AAE15347 Aae15347 Human imm
9	1225	97.2 232 5 AAE26272 Aae26272 Human IGG
10	1225	97.2 232 7 ADJ65991 Adj65991 Herpes vi
11	1225	97.2 232 8 ADJ57512 Adj57512 Human IgG
12	1225	97.2 232 8 ADR48992 Adr48992 Human IgG
13	1225	97.2 233 5 ABB09463 Abb09463 Human IgG
14	1225	97.2 235 6 ADA89055 Ada89055 Human IgG
15	1225	97.2 235 7 ADD25647 Add25647 Binding d
16	1225	97.2 235 7 ADG74307 Adg74307 Fibroblast
17	1225	97.2 247 5 AAE26274 Aae26274 Human bet
18	1225	97.2 251 5 ABB81490 Abb81490 Human imm
19	1225	97.2 251 6 AAE82514 Aae82514 Human wil
20	1225	97.2 259 2 AYV24154 AYV24154 Protein F
21	1225	97.2 267 5 AAB26273 Aae26273 Human tPA
22	1225	97.2 269 8 ADJ51200 Adj51200 CH1 dele
23	1225	97.2 287 4 AAB47590 Ab47590 Fusion pr
24	1225	97.2 329 2 AAR91806 Aar91806 Human imm
<b>ALIGNMENTS</b>		
RESULT	ID	RESUIT 1
XX	XX	AAO19665 standard; protein; 232 AA.
AC	XX	AAO19665;
XX	DT	28-MAR-2003 (first entry)
XX	DE	Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.
XX	KW	Human; IgG1; immunoglobulin G; immunotherapy; immune disease; Fc epsilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; antiarthritic; antirheumatic; antidiabetic; neuroprotective; hinge-CH2-CH3 region.
XX	OS	Homo sapiens.
XX	PN	WO200288317-A2.
XX	PD	07-NOV-2002.
XX	PP	01-MAY-2002; 2002WO-US013527.
XX	PR	01-MAY-2001; 2001US-00847208.
XX	PR	24-OCT-2001; 2001US-00000439.
XX	PA	(REGC ) UNIV CALIFORNIA.
XX	PI	Saxon A, Zhang K, Zhu D;
XX	DR	WPI; 2003-103456/09.
XX	PT	New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgG receptor, useful for treating IgG mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.
XX	PT	Claim 19; Fig 3; 116pp; English.
CC	CC	The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgG receptor (Fc epsilon receptor). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for

CC treating an IgG-mediated biological response, preferably an IgG-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type I diabetes mellitus, or multiple sclerosis, and for preventing off, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgG1 heavy chain constant region hinge-CH2-CH3 portion

SQ Sequence 232 AA;

Query Match 100.0%; Score 1260; DB 6; Length 232; Best Local Similarity 100.0%; Pred. No. 2.98-91; Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCPPCPAPELIGGSPVFLFPPKPKOTLMISRPEVTCVVVDVSHDPEVKF 60  
Db 61 NWYVDGVEVIRNKTKPREEQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPPIKT 120  
61 EPKSCDKTHCPPCPAPELIGGSPVFLFPPKPKOTLMISRPEVTCVVVDVSHDPEVKF 60  
Qy 121 ISKAKVQPREQVYLPPSDELTNQVSITCLVKGFPYSDIAVEWESNGOPENNYKTP 180  
121 ISKAKVQPREQVYLPPSDELTNQVSITCLVKGFPYSDIAVEWESNGOPENNYKTP 180  
Db 181 PVLDVGSGFPLYSKLTVDKSRSRQGNVFSVMMHEALTHHNYQORSLSLSPGK 232  
181 PVLDVGSGFPLYSKLTVDKSRSRQGNVFSVMMHEALTHHNYQORSLSLSPGK 232

RESULT 2

ID AAO19664 standard; protein; 330 AA.  
XX AAO19664;

AC AAO19664;  
XX DT 28-MAR-2003 (first entry)

DE Human IgG1 heavy chain constant region.

XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease; Fc epsilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; antiarthritic; antirheumatic; antidiabetic; neuroprotective.

OS Homo sapiens.

XX WO200288317-A2.

XX 01-MAY-2001; 2001US-00847208.

XX PR 24-OCT-2001; 2001US-00000439.  
XX PA (REGC ) UNIV CALIFORNIA.

XX PI Saxon A, Zhang K, Zhu D,  
XX DR WPI; 2003-103456/09.

XX New fusion molecules comprising polypeptide sequences that bind to IgG PT inhibitory receptor and native IgG receptor, useful for treating IgG- PT mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

XX Claim 64; Fig 2; 116pp; English.

CC The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG

CC inhibitory receptor consisting of an immune receptor tyrosine-based CC inhibitor motif (ITIM), expressed on mast cells, basophils or B cell, CC functionally connected to a second polypeptide sequence capable of CC specific binding directly or indirectly to a native IgG receptor CC (FcpsilonR). Also provided are nucleotide sequences encoding such a CC fusion protein. The fusion molecules and compositions are useful for CC treating an IgG-mediated biological response, preferably an IgG-mediated CC hypersensitivity reaction such as asthma, allergic rhinitis, atopic CC dermatitis, severe food allergies, chronic urticaria, angioedema or CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, CC type-I diabetes mellitus, or multiple sclerosis, and for preventing off, CC or symptoms resulting from, a type I hypersensitivity reaction in a CC subject receiving immunotherapy. The present sequence is the human IgG1 CC heavy chain constant region

SQ Sequence 330 AA;

Query Match 100.0%; Score 1260; DB 6; Length 330; Best Local Similarity 100.0%; Pred. No. 4.48-91; Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCPPCPAPELIGGSPVFLFPPKPKOTLMISRPEVTCVVVDVSHDPEVKF 60  
Db 99 EPKSCDKTHCPPCPAPELIGGSPVFLFPPKPKOTLMISRPEVTCVVVDVSHDPEVKF 158  
Qy 61 NWYVDGVEVIRNKTKPREEQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPPIKT 120  
61 EPKSCDKTHCPPCPAPELIGGSPVFLFPPKPKOTLMISRPEVTCVVVDVSHDPEVKF 60  
Db 159 NWYVDGVEVIRNKTKPREEQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPPIKT 218  
Qy 121 ISKAKVQPREQVYLPPSDELTNQVSITCLVKGFPYSDIAVEWESNGOPENNYKTP 180  
121 ISKAKVQPREQVYLPPSDELTNQVSITCLVKGFPYSDIAVEWESNGOPENNYKTP 180  
Db 219 ISKAKVQPREQVYLPPSDELTNQVSITCLVKGFPYSDIAVEWESNGOPENNYKTP 278  
219 ISKAKVQPREQVYLPPSDELTNQVSITCLVKGFPYSDIAVEWESNGOPENNYKTP 278  
Qy 181 PVLDVGSGFPLYSKLTVDKSRSRQGNVFSVMMHEALTHHNYQORSLSLSPGK 232  
181 PVLDVGSGFPLYSKLTVDKSRSRQGNVFSVMMHEALTHHNYQORSLSLSPGK 232  
Db 279 PVLDVGSGFPLYSKLTVDKSRSRQGNVFSVMMHEALTHHNYQORSLSLSPGK 330

RESULT 3

ID AAO19668 standard; protein; 569 AA.  
XX AAO19668;

AC AAO19668;  
XX DT 28-MAR-2003 (first entry)

DE GE2 fusion protein for use in treating immune diseases.

XX Human; IgE; immunoglobulin E; immunotherapy; immune disease; Fc epsilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2; antiarthritic; antirheumatic; antidiabetic; neuroprotective; fusion protein.

XX OS Synthetic;  
OS Unidentified.  
XX WO200288317-A2.  
XX PN 07-NOV-2002.  
XX PD 01-MAY-2002; 2002WO-US013527.  
XX PR 01-MAY-2001; 2001US-00847208.  
XX PR 24-OCT-2001; 2001US-00000439.  
XX PA (REGC ) UNIV CALIFORNIA.

XX PI Saxon A, Zhang K, Zhu D,  
XX DR WPI; 2003-103456/09.

XX New fusion molecules comprising polypeptide sequences that bind to IgG PT inhibitory receptor and native IgG receptor, useful for treating IgG- PT mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

XX Claim 64; Fig 2; 116pp; English.

CC The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG

PT inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

XX  
PT  
XX  
PS Claim 35; Fig 7; 116pp; English.

CC The present invention relates to a fusion molecule comprising a first CC polypeptide sequence capable of specific binding to a native IgG CC inhibitory receptor consisting of an immune receptor tyrosine-based CC functionally connected to a second polypeptide sequence capable of CC specific binding directly or indirectly to a native IgE receptor (Fc epsilon R). Also provided are nucleotide sequences encoding such a CC fusion protein. The fusion molecules and compositions are useful for CC treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic CC dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of, CC or symptoms resulting from, a type I hypersensitivity reaction in a CC subject receiving immunotherapy. The present sequence is a gamma hinge- CC Chgamma2-CHgamma3-(Gly4Ser)3-Chepsilon1-Chepsilon1-3-Chepsilon1 fusion CC protein (designated GE2) of the invention

XX  
Sequence 569 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	100.0%	6	569
Matches	Conservative	100.0%		
	Mismatches	0		
	Indels	0		
	Gaps	0		

QY 1 EPKSCDKTHTCPPCPAPELIGGSPVLFPPPKPDTLMISITPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKTHTCPPCPAPELIGGSPVLFPPPKPDTLMISITPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYDVGVEVINKTKTKEPREQNSTRVWSUTLVQVWAMKEYKCKVSKNKLAPIKT 120  
Db 61 NWYDVGVEVINKTKTKEPREQNSTRVWSUTLVQVWAMKEYKCKVSKNKLAPIKT 120  
QY 121 ISAKAQOPRERPVQVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISAKAQOPRERPVQVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
QY 181 PVLDGSFFPLYSKLTVDKSRWQQNVFSGSVMMHALHNHYQQRSLSLSPGK 232  
Db 181 PVLDGSFFPLYSKLTVDKSRWQQNVFSGSVMMHALHNHYQQRSLSLSPGK 232

RESULT 4  
AAW26232  
ID AAW26232 standard; protein; 232 AA.

AC AAW26232;  
XX DT 16-MAR-1998 (first entry)

XX DB Human IgG1 hinge/Fc region.

XX KW Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.  
XX OS Homo sapiens.

XX PN WO9728272-A1.

XX PD 07-AUG-1997.

XX PP 31-JAN-1997; 97WO-US001470.

XX PR 31-JAN-1996; 96US-00595043.

XX PA (TECH-) TECHNOLOGENE INC.

XX PI Sgarlato GD;

XX DR WPI; 1997-402624/37.  
XX N-PSDB; AT80158.

XX PT Recombinant protein expression system for fusion protein production -  
XX PT useful for high quantity production of authentic recombinant proteins.

XX PS Example 3; Page 133-134; 194pp; English.

CC A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein CC comprises three domains joined together in order, from N-terminus to C-terminus, of a first domain comprising a protein of interest, a second CC domain comprising a hydrophilic spacer and an affinity domain, each CC domain comprising amino acid residues. The present sequence represents CC the hinge/Fc region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic CC recombinant proteins of interest. The method of the invention is useful CC for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the CC efficient cleavage and generation of authentic proteins of interest that CC do not contain extraneous (i.e. non-naturally occurring) amino acids

XX SQ Sequence 232 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	97.0%	2	232
Matches	Conservative	3		
	Mismatches	4		
	Indels	0		
	Gaps	0		

QY 1 EPKSCDKTHTCPPCPAPELIGGSPVLFPPPKPDTLMISITPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKTHTCPPCPAPELIGGSPVLFPPPKPDTLMISITPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYDVGVEVINKTKTKEPREQNSTRVWSUTLVQVWAMKEYKCKVSKNKLAPIKT 120  
Db 61 NWYDVGVEVINKTKTKEPREQNSTRVWSUTLVQVWAMKEYKCKVSKNKLAPIKT 120  
QY 121 ISAKAQOPRERPVQVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISAKAQOPRERPVQVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
QY 181 PVLDGSFFPLYSKLTVDKSRWQQNVFSGSVMMHALHNHYQQRSLSLSPGK 232  
Db 181 PVLDGSFFPLYSKLTVDKSRWQQNVFSGSVMMHALHNHYQQRSLSLSPGK 232

RESULT 5  
AAB28690

ID AAB28690 standard; protein; 232 AA.  
XX AC AAB28690;  
XX DT 14-FEB-2001 (first entry)

XX DE Human IgGammal hinge, CH2 and CH3 regions.  
XX KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis; IgGammal.  
XX OS Homo sapiens.

XX PN WO200063253-A1.  
XX PD 26-OCT-2000.  
XX PP 24-MAR-2000; 2000WO-US008004.  
XX PR 16-APR-1999; 99US-00293245.

XX PI

PA (AMGE-) AMGEN INC.  
 XX  
 PT Hsu H, Meng S;  
 XX  
 DR WPI; 2000-66240/64.  
 XX  
 PT Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.  
 XX  
 PS Claim 2; Fig 1; 93pp; English.

XX  
 CC The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an Fc immunoglobulin region fused to the N-terminal portion of the AGP-1 protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies.

XX  
 SQ Sequence 232 AA;

Query	Match	Best Local Similarity	Score	DB	Length
	97.2%	97.0%	1225	3	232
Matches	225;	Conservative	Pred.	No.	1.7e-88;
	3;	Mismatches			4;
		Indels			0;
		Gaps			0;

QY 1 EPKSDKTHTCPPCCAPELIGGSPVLFPPPKPDKLMSRTPETCVVVVSHSEPEVKF 60  
 Db 1 EPKSDKTHTCPPCCAPELIGGSPVLFPPPKPDKLMSRTPETCVVVVSHSEPEVKF 60  
 QY 61 NWYVGVEVNVKKTPREEQYNSTRVVSLTVLQVNWNNWNGKEYKCKVSNAKALAPIKT 120  
 Db 61 NWYVGVEVNVKKTPREEQYNSTRVVSLTVLQVNWNNWNGKEYKCKVSNAKALAPIKT 120  
 QY 61 NWYVGVEVNVKKTPREEQYNSTRVVSLTVLQVNWNNWNGKEYKCKVSNAKALAPIKT 120  
 Db 61 NWYVGVEVNVKKTPREEQYNSTRVVSLTVLQVNWNNWNGKEYKCKVSNAKALAPIKT 120  
 QY 121 ISKAKVQPREPQVTLPPSRDELTKNQSVITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Db 121 ISKAKVQPREPQVTLPPSRDELTKNQSVITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 QY 181 PVLDVGSEFLYSKLTVDKSRWQCNVFSCSVMHEALHNHYTQKSLISPGK 232  
 Db 181 PVLDVGSEFLYSKLTVDKSRWQCNVFSCSVMHEALHNHYTQKSLISPGK 232  
 QY 181 PVLDVGSEFLYSKLTVDKSRWQCNVFSCSVMHEALHNHYTQKSLISPGK 232  
 Db 181 PVLDVGSEFLYSKLTVDKSRWQCNVFSCSVMHEALHNHYTQKSLISPGK 232

RESULT 6  
 AAB80897  
 ID AAB80897 standard; protein; 232 AA.  
 XX  
 AC AAB80897;  
 XX  
 DT 31-MAY-2001 (first entry)  
 XX  
 DE Human IgGammal hinge, CH<sub>2</sub> and CH<sub>3</sub> regions.

XX  
 Human; IgGammal; anticancer; Antimetastatic; Osteogenic; Lytic bone disease; multiple myeloma; immunoglobulin; osteosclerotic bone metastasis; Opg; osteoprotegerin; osteoclast formation inhibition; bone resorption inhibition. Homo sapiens.

XX  
 WO200117543-A2.

PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US022806.  
 XX  
 PR 03-SEP-1999; 99US-00389545.  
 XX  
 PA (AMGE-) AMGEN INC.

XX  
 Dunstan CR;  
 XX  
 DR WPI; 2001-265936/27.  
 XX  
 PT Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegerin polypeptide.  
 XX  
 PS Disclosure; Fig 1; 87pp; English.

XX  
 CC The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegerin) polypeptide or OPG fusion protein. The OPG proteins (see AAB80897; ABB0905) can inhibit formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence is the hinge, CH<sub>2</sub> and CH<sub>3</sub> regions of human IgGammal. This sequence can be used to generate fusion proteins of OPG and immunoglobulin, for use in the present invention. The generated fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity.

XX  
 SQ Sequence 232 AA;

Query	Match	Best Local Similarity	Score	DB	Length
	97.2%	97.0%	1225	4	232
Matches	225;	Conservative	Pred.	No.	1.7e-88;
	3;	Mismatches			4;
		Indels			0;
		Gaps			0;

QY 1 EPKSDKTHTCPPCCAPELIGGSPVLFPPPKPDKLMSRTPETCVVVVSHSEPEVKF 60  
 Db 1 EPKSDKTHTCPPCCAPELIGGSPVLFPPPKPDKLMSRTPETCVVVVSHSEPEVKF 60  
 QY 61 NWYVGVEVNVKKTPREEQYNSTRVVSLTVLQVNWNNWNGKEYKCKVSNAKALAPIKT 120  
 Db 61 NWYVGVEVNVKKTPREEQYNSTRVVSLTVLQVNWNNWNGKEYKCKVSNAKALAPIKT 120  
 QY 121 ISKAKVQPREPQVTLPPSRDELTKNQSVITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Db 121 ISKAKVQPREPQVTLPPSRDELTKNQSVITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 QY 181 PVLDVGSEFLYSKLTVDKSRWQCNVFSCSVMHEALHNHYTQKSLISPGK 232  
 Db 181 PVLDVGSEFLYSKLTVDKSRWQCNVFSCSVMHEALHNHYTQKSLISPGK 232

RESULT 7  
 AAY2915  
 ID AAY2915 standard; protein; 232 AA.  
 XX  
 AC AAY2915;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX  
 DE Human partial IgG1 protein comprising hinge, CH<sub>2</sub> and CH<sub>3</sub> regions.

XX  
 Human; fusion protein; osteoprotgerin; OPG; Fc protein; osteopathic; therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis; hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis; osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1; periodontal. Homo sapiens.

XX  
 WO200118203-A1.

PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US022797.  
 XX  
 PR 03-SEP-1999; 99US-00389782.  
 XX  
 PA (AMGE-) AMGEN INC.

XX Dunstan CR, Wooden SK, Mann MB;

XX WPI; 2001-244572/25.

DR

PT

DR WPI; 2002-034433/04.

XX Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.

XX Example 1; Fig 10; 95pp; English.

XX Sequence 232 AA:

Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGPGPSVFLFPKPKDTLIMISRTPETVCVVVDVSHEDPEVK 60  
Db 1 EPKSCDKTHTCPPCPAPELLGPGPSVFLFPKPKDTLIMISRTPETVCVVVDVSHEDPEVK 60

QY 61 NWYVGVEVINKTKPREEQYNSTRVSVLTVLHQWMMGKEYKKVSKNKLAPIKT 120  
Db 61 NWYVGVEVINKTKPREEQYNSTRVSVLTVLHQWMMGKEYKKVSKNKLAPIKT 120

QY 121 ISAKVQPREQVYTLPPSDELTKNQVSITCLVKGFPYSFSDIAVIEWSNGOPENNYKTP 180  
Db 121 ISAKVQPREQVYTLPPSDELTKNQVSITCLVKGFPYSFSDIAVIEWSNGOPENNYKTP 180

QY 181 PVLDVGSGFFLYSKLTVDKSRWQGVFSCSVVMHEALTHNHYQRSLSLSPGK 232  
Db 181 PVLDVGSGFFLYSKLTVDKSRWQGVFSCSVVMHEALTHNHYQRSLSLSPGK 232

RESULT 8 AAE15347

ID AAE15347 standard; protein; 232 AA.

AC AAE15347;

XX

DT 09-APR-2002 (first entry)

XX Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.

XX Human; erythropoietin; Epo; haemocrit; anaemia; kidney function; IgG; cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.

OS Homo sapiens.

XX WO200181405-A2.

XX 01-NOV-2001.

XX 19-APR-2001; 2001WO-US012836.

XX 21-APR-2000; 2000US-00559001.

XX (AMGE-) AMGEN INC.

XX Egrie JC, Elliott SG, Browne JK, Sitney KC;

PR 29-NOV-2000; 2000US-0253302P.

PR 29-NOV-2000; 2000US-0250198P.

DR WPI; 2002-034433/04.

XX The invention relates to a method for increasing and maintaining haemocrit in a mammal. The method comprises administering a hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical composition, less frequently than an equivalent molar amount of and at a lower molar amount than recombinant human Epo (rhEpo) to obtain a comparable target haemocrit. Epo is a glycoprotein hormone necessary for the maturation of erythroid progenitor cells into erythrocytes. Human Epo analogue is useful for raising and maintaining haemocrit to a comparable target haemocrit in a mammal suffering from anaemia associated with a decline or loss of kidney function, myelosuppressive therapy comprising chemotherapeutic or anti-viral drugs or associated with excessive blood loss during surgical procedures, and in cancer condition. The present sequence is human immunoglobulin G (IgG) gamma 1 constant heavy chain (CH2, CH3) hinge region used to construct Epo hyperglycosylated analogue fusion protein.

XX Sequence 232 AA:

Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGPGPSVFLFPKPKDTLIMISRTPETVCVVVDVSHEDPEVK 60  
Db 1 EPKSCDKTHTCPPCPAPELLGPGPSVFLFPKPKDTLIMISRTPETVCVVVDVSHEDPEVK 60

QY 61 NWYVGVEVINKTKPREEQYNSTRVSVLTVLHQWMMGKEYKKVSKNKLAPIKT 120  
Db 61 NWYVGVEVINKTKPREEQYNSTRVSVLTVLHQWMMGKEYKKVSKNKLAPIKT 120

QY 121 ISAKVQPREQVYTLPPSDELTKNQVSITCLVKGFPYSFSDIAVIEWSNGOPENNYKTP 180  
Db 121 ISAKVQPREQVYTLPPSDELTKNQVSITCLVKGFPYSFSDIAVIEWSNGOPENNYKTP 180

QY 181 PVLDVGSGFFLYSKLTVDKSRWQGVFSCSVVMHEALTHNHYQRSLSLSPGK 232  
Db 181 PVLDVGSGFFLYSKLTVDKSRWQGVFSCSVVMHEALTHNHYQRSLSLSPGK 232

RESULT 9 AAB26272

ID AAB26272 standard; protein; 232 AA.

AC AAB26272;

XX

DT 14-NOV-2002 (first entry)

XX Human IgG1 heavy chain.

XX Human; amyloid protein; Alzheimer's disease; Huntington's disease; spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis; Gerstmann-Sträussler-Scheinker syndrome; spongiform encephalopathy; GSS; Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma; CJ.

OS Homo sapiens.

XX WO200242462-A2.

XX 30-MAY-2002.

XX 27-NOV-2001; 2001WO-US044581.

XX 27-NOV-2000; 2000US-0253302P.

PR 29-NOV-2000; 2000US-0250198P.



XX	OS	Homo sapiens.
XX	KW	antihaemetic; nephrotoxic; human; HuEPO-L-VFC; erythropoietin; EPO;
XX	KW	anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
XX	KW	AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
PD	XX	OS
PD	XX	Homo sapiens.
22-JAN-2004.	XX	US2004175324-A1.
PR	XX	09-JUL-2003; 2003WO-DK000481.
PR	XX	12-JUL-2002; 2002DK-0001099.
XX	PA	(NOVO ) NOVO NORISK AS.
XX	PI	Bjorn SE, Nicolaisen EM, Steenstrup TD;
XX	DR	WPI; 2004-180224/17.
XX	PT	New compound binding to tissue factor, useful for treating diseases such as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
XX	PS	Claim 16; SEQ ID NO 7; 61pp; English.
XX	CC	The invention relates to a compound (I) binding to tissue factor (TF).
CC	CC	The compound (I) has the formula A-(Lm)-C, where A is a FVIIa polypeptide, Lm is an optional linker group, C comprises an immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-mediated activated factor VII (FVIIa) activity. (I) is useful as a medicament, and for the manufacture of a medicament for preventing or treating disease or disorder associated with pathophysiological TF activity. The disease or disorder associated with pathophysiological TF activity are deep venous thrombosis, arterial thrombosis, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal coronary angioplasty (PTCA), stroke, cancer, tumor metastasis, angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis, arteriosclerosis and restenosis following angioplasty, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial infarction, or prophylactic treatment of mammals with atherosclerotic vessels at risk for thrombosis. The present sequence represents the Fc domain fragment of human immunoglobulin G1 (IgG1).
XX	SO	Sequence 232 AA;
Query Match	Best Local Similarity	97.2%; Score 1225; DB 8; Length 232;
Matches	225; Conservative	97.0%; Pred. No. 1.7e-88; Length 225; Mismatches 3; Indels 0; Gaps 0;
Oy	1	EPKSCKHTCPCCPAPELGGPSVLFPEPKPOTLMISRTPEVTCWVVDVSHDPEVKF 60
Db	1	EPKSCKHTCPCCPAPELGGPSVLFPEPKPOTLMISRTPEVTCWVVDVSHDPEVKF 60
Oy	61	NWYVTDGVEHNVKTKPREQYNSTYRVWSLTWQHQNMNGKEKKVSKNKAQAPIKT 120
Db	61	NWYVTDGVEHNVKTKPREQYNSTYRVWSLTWQHQNMNGKEKKVSKNKAQAPIKT 120
Oy	121	ISKAKVQPREQQVTLPPSERDELTRKNQVSLTCLYKGYPFDIANEWESNQPNENYKTP 180
Db	121	ISKAKVQPREQQVTLPPSERDELTRKNQVSLTCLYKGYPFDIANEWESNQPNENYKTP 180
Oy	181	PVLDSVGSPFLYSLTVKSRWQCGNVSQSCVMEALHNHQQSIISLRPK 232
Db	181	PVLDSVGSPFLYSLTVKSRWQCGNVSQSCVMEALHNHQQSIISLRPK 232
RESULT 12	ADR4892	ADR4892 standard; peptide; 232 AA.
ID	ADR4892	ADR4892; AC 02-DEC-2004 (first entry)
XX	AC	Human IgG1 hinge and CH2 region.

CC or kidney was used as the template in polymerase chain reaction (PCR).  
 CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a  
 CC restriction enzyme cleavage site is used as the 5' oligonucleotide  
 CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon  
 CC and incorporates a BamHI site.  
 CC approximately 600 bp were inserted into a holding vector such as pUC19 at  
 CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the  
 CC human EPO gene was confirmed by DNA sequencing.

XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.7e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHICPPCPAPELIGGSPVLPFPKPDKTLMISRTPETCWWVVDVSHEDPEVKF 60  
 Db 1 EPKSCDKTHICPPCPAPELIGGSPVLPFPKPDKTLMISRTPETCWWVVDVSHEDPEVKP 60  
 QY 61 NWYUDGVENVNKVKPREEQNSTTRVSVLTVLHQWNGKEYKCKVSNKALPPIKT 120  
 61 NWYUDGVENVNKVKPREEQNSTTRVSVLTVLHQWNGKEYKCKVSNKALPPIKT 120  
 Db 121 ISAKAQPREPVYLPPSDELTKNQVSITCLVKGFYPSDIAVEWESQOPENNYKTP 180  
 121 ISAKAQPREPVYLPPSDELTKNQVSITCLVKGFYPSDIAVEWESQOPENNYKTP 180  
 Db 181 PVLDVGSGFLYKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232  
 181 PVLDVGSGFLYKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232  
 QY 181 PVLDVGSGFLYKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232  
 Db 182 PVLDSDGSFFLYSKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232  
 182 PVLDSDGSFFLYSKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232

RESULT 13

ABB09463  
 ID ABB09463 standard; protein; 233 AA.  
 AC ABB09463;  
 XX DT 01-JUL-2002 (first entry)  
 DE Human IgG Fc fragment amino acid sequence.

XX Protein A; immunoglobulin G; IgG; antibody; human.  
 KW Homo sapiens.

XX Key' Location/Qualifiers  
 FT Misc-difference 168 /note= "encoded by GAC"  
 FT Misc-difference 169 /note= "encoded by ACC"

XX WO200204602-A1.  
 XX PD 17-JAN-2002.  
 XX PP 04-JUL-2001; 2001WO-JP005788.  
 XX PR 07-JUL-2000; 2000JP-00206689.  
 XX PA (GENC-) GENCOM CORP.  
 XX PI Tanaka, A., Ueda M., Teranishi Y.;  
 XX DR WPI; 2002-148174/19.  
 XX DR N-RSDB; ABL52834.

XX

PT Transformant yeast for stable supply of highly active catalytic antibody,  
 PT comprises the capability of expressing and presenting protein A or its  
 PT fragment, particularly with the ZZ domain, on the cell surface.

XX Example 3; Fig 4; 25pp; Japanese.

CC The invention relates to a transformant yeast that can present protein A  
 CC or its fragment on its cell surface. The yeast can be used for detecting  
 CC or isolating the Fc part of immunoglobulin (IgG). The yeast is useful for  
 CC a stable supply of highly active catalytic antibody e.g. by screening  
 CC novel functional molecules and in isolating Fc-carrying secretory  
 CC proteins. The yeast of the invention is capable of adhering specifically  
 CC to a combinatorial antibody library with an Fc-carrying antibody  
 CC component. The current sequence represents the human IgG Fc fragment  
 CC amino acid sequence.

XX Sequence 233 AA;

Query Match 97.2%; Score 1225; DB 5; Length 233;  
 Best Local Similarity 97.0%; Pred. No. 1.7e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHICPPCPAPELIGGSPVLPFPKPDKTLMISRTPETCWWVVDVSHEDPEVKF 60  
 Db 2 EPKSCDKTHICPPCPAPELIGGSPVLPFPKPDKTLMISRTPETCWWVVDVSHEDPEVKF 61  
 QY 61 NWYUDGVENVNKVKPREEQNSTTRVSVLTVLHQWNGKEYKCKVSNKALPPIKT 120  
 62 NWYUDGVENVNKVKPREEQNSTTRVSVLTVLHQWNGKEYKCKVSNKALPPIKT 121  
 Db 121 ISAKAQPREPVYLPPSDELTKNQVSITCLVKGFYPSDIAVEWESQOPENNYKTP 180  
 122 ISAKAQPREPVYLPPSDELTKNQVSITCLVKGFYPSDIAVEWESQOPENNYKTP 181  
 Db 181 PVLDVGSGFLYKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232  
 182 PVLDSDGSFFLYSKLTVDKSRWQGNVFSVMSMHALHNHYQQRSLSLSGK 232

RESULT 14

ABJ38647  
 ID ABJ38647 standard; protein; 235 AA.  
 AC ABJ38647;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE PCXFC protein SEQ ID NO 6.

XX Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;  
 KW antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;  
 KW constitutive activation; chondrocytes; cell Proliferative disorder;  
 KW achondroplasia; thanatophoric dysplasia; acanthosis nigricans; dysplasia;  
 KW hypochondroplasia; severe achondroplasia; transitional cell carcinoma;  
 KW Muieke coronal craniosynostosis; Crowne syndrome; acanthosis nigricans;  
 KW tumour progression; osteosarcoma; chordosarcoma; multiple myeloma;  
 KW mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein;  
 XX OS Homo sapiens.  
 XX WO2002102854-A2.  
 XX PN WO2002102854-A2.  
 XX PD 27-DEC-2002.  
 XX PR 20-JUN-2002; 2002WO-1B003523.  
 XX PR 20-JUN-2001; 2001US-0299187P.  
 XX PR (MORB-) MORPHOSYS AG.  
 XX PR (PROC-) PROCHON BIOTECH LTD.  
 XX PI Thomasen-Wolf, B., Borges, E., Yayon, A., Rom, E.;  
 XX DR WPI; 2003-167489/16.  
 XX DR N-PADB; ABT40262.

PT activation of receptor protein tyrosine kinase, useful for treating or  
 PT inhibiting skeletal dysplasias, Craniosynostosis or cell proliferative  
 XX

(PROC-) PROCHON BIOTECH LTD.  
Yayon A, Rom E;  
WPI; 2003-175236/17.  
N-PSDB; ADA89054.

New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of RPTK, useful for treating bone and cartilage disorders, or malignant cell proliferative diseases.

Example 2; Page 43; 122pp; English.

Tue Jun 7 11:11:11 2005

us-10-000-439-3.open.rag

Page 10

Db 124 ISKAKQPREPQVYILPPSRBLTKNQVSLTCLVKCFPSDIANEWSNGOPENNYKTP 183  
Qy 181 PVLUSVGSEFLYSKLTVDKSERWQGNVFSCSVMHALHNHYQQRSLSPGK 232  
||| ||| ||| ||| ||| ||| ||| : ||| ||| |||  
Db 184 PVLUSDGSEFLYSKLTVDKSERWQGNVFSCSVMHALHNHYQQRSLSPGK 235

Search completed: June 7, 2005, 08:56:39  
Job time : 119.83 secs

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## Om protein - protein search, using sw model

Run on:

June 7, 2005, 09:01:44 ; Search time 101.775 seconds  
 (without alignments)

821.093 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHICPPCPAPLL.....MHEALHNHYQRSLSLSPGK 232

Scoring table: BloSUM62

Ggap 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	DB ID	Description	Best Local Similarity	Score	DB 10;	Length	232;	Sequence 26, Appi
1	1260	100.0	232	10 US-09-847-208-3	Sequence 3, Appli	100.0%; Pred. No. 9.8e-93;	Score 1260; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
2	1260	100.0	232	14 US-10-000-439-3	Sequence 3, Appli	100.0%; Pred. No. 9.8e-93;	Score 1260; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
3	1260	100.0	330	10 US-09-847-208-2	Sequence 2, Appli	100.0%; Pred. No. 9.8e-93;	Score 1260; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
4	1260	100.0	330	14 US-10-000-439-2	Sequence 2, Appli	100.0%; Pred. No. 9.8e-93;	Score 1260; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
5	1260	100.0	569	10 US-09-847-208-7	Sequence 7, Appli	100.0%; Pred. No. 9.8e-93;	Score 1260; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
6	1260	100.0	569	14 US-10-000-439-7	Sequence 7, Appli	100.0%; Pred. No. 9.8e-93;	Score 1260; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
7	1225	97.2	232	9 US-09-996-357-10	Sequence 1, Appli	97.2%; Pred. No. 9.8e-93;	Score 1225; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
8	1225	97.2	232	10 US-09-389-782-1	Sequence 1, Appli	97.2%; Pred. No. 9.8e-93;	Score 1225; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
9	1225	97.2	232	16 US-10-617-619-7	Sequence 7, Appli	97.2%; Pred. No. 9.8e-93;	Score 1225; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
10	1225	97.2	232	16 US-10-761-593A-26	Sequence 26, Appli	97.2%; Pred. No. 9.8e-93;	Score 1225; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
11	1225	97.2	232	16 US-10-831-622-97	Sequence 97, Appli	97.2%; Pred. No. 9.8e-93;	Score 1225; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi
12	1225	97.2	232	16 US-10-800-497-26	Sequence 26, Appli	97.2%; Pred. No. 9.8e-93;	Score 1225; DB 10;	Length 232;	Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 26, Appi

## ALIGNMENTS

## RESULT 1

US-09-847-208-3

; Sequence 3, Application US-09847208

; Publication No. US20030082190A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; APPLICANT: Zhang, Ke

; APPLICANT: Zhu, Daocheng

; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

FILE REFERENCE: UC67 002A

CURRENT APPLICATION NUMBER: US/09/847,208

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FastSEQ For Windows Version 4.0

SEQ ID NO 3

LENGTH: 232

TYPE: PRT

ORGANISM: Homo sapiens

US-09-847-208-3

Query Match length 100.0%; Score 1260; DB 10; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-93;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHICPPCPAPLLGGPSVFLPKPKPDKLMTSRPTPEYTCWVWDVSHPDEVK 60  
 Db 1 EPKSCDKTHICPPCPAPLLGGPSVFLPKPKPDKLMTSRPTPEYTCWVWDVSHPDEVK 60

Qy 121 ISAKVQPREPVVYLPPSPRDELTKNQVSLTCLVKGFYSSDIAYEWESNGQOPENNIKTP 180  
 Db 61 NWYDVGVEVHVKTKPREGSYNTVRWVSLTVLHQNMNGKEYCKVSKNKPALPIKT 120

RESULT 2  
US-10-000-439-3  
; Sequence 3, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000, 439  
; CURRENT FILING DATE: 2001-10-24  
; PRIORITY APPLICATION NUMBER: US 09/847, 208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ For Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-000-439-3

Query Match 100.0%; Score 1260; DB 14; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9.8e-93; Mismatches 0; Indels 0; Gaps 0;  
Matches 232; Conservative 0; MisMatches 0; InDelS 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPELIGGSPVFLFPPKPKDLMISRTPEVTCVVVDVSHDPEVKF 60  
Db 1 EPKSCDKTHTCPPCAPELIGGSPVFLFPPKPKDLMISRTPEVTCVVVDVSHDPEVKF 60

QY 1 ISKAKVQPRPQQVTLPSSRDELTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISKAKVQPRPQQVTLPSSRDELTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180

QY 181 PVLDVGSGFFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYQORSLSLSPGK 232  
Db 181 PVLDVGSGFFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYQORSLSLSPGK 232

RESULT 3  
US-09-847-208-2  
; Sequence 2, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Dacheng  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
; FILE REFERENCE: UC67.002A  
; CURRENT APPLICATION NUMBER: US/09/847, 208  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSEQ For Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-847-208-2

Query Match 100.0%; Score 1260; DB 10; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.8e-92; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPELIGGSPVFLFPPKPKDLMISRTPEVTCVVVDVSHDPEVKF 60  
Db 99 EPKSCDKTHTCPPCAPELIGGSPVFLFPPKPKDLMISRTPEVTCVVVDVSHDPEVKF 158

QY 61 NWYUDGVEVNWKTPREEQYNSTYRVSVLTUHQNMNGKEYKCKVSKNALPAPIKT 120  
Db 61 NWYUDGVEVNWKTPREEQYNSTYRVSVLTUHQNMNGKEYKCKVSKNALPAPIKT 120

QY 121 ISKAKVQPRPQQVTLPSSRDELTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISKAKVQPRPQQVTLPSSRDELTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180

QY 181 PVLDVGSGFFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYQORSLSLSPGK 232  
Db 181 PVLDVGSGFFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYQORSLSLSPGK 232

RESULT 4  
US-10-000-439-2  
; Sequence 2, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000, 439  
; CURRENT FILING DATE: 2001-10-24  
; PRIORITY APPLICATION NUMBER: US 09/847, 208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ For Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-000-439-2

Query Match 100.0%; Score 1260; DB 14; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.5e-92; Mismatches 0; Indels 0; Gaps 0;  
Matches 232; Conservative 0; MisMatches 0; InDelS 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPELIGGSPVFLFPPKPKDLMISRTPEVTCVVVDVSHDPEVKF 60  
Db 99 EPKSCDKTHTCPPCAPELIGGSPVFLFPPKPKDLMISRTPEVTCVVVDVSHDPEVKF 158

QY 61 NWYUDGVEVNWKTPREEQYNSTYRVSVLTUHQNMNGKEYKCKVSKNALPAPIKT 120  
Db 159 NWYUDGVEVNWKTPREEQYNSTYRVSVLTUHQNMNGKEYKCKVSKNALPAPIKT 218

QY 121 ISKAKVQPRPQQVTLPSSRDELTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTP 180  
Db 219 ISKAKVQPRPQQVTLPSSRDELTKNQSLTCLVKGFPSDIAVEWESNGOPENNYKTP 278

QY 181 PVLDVGSGFFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYQORSLSLSPGK 232  
Db 279 PVLDVGSGFFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYQORSLSLSPGK 330

NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSEQ For Windows Version 4.0  
; SEQ ID NO: 7  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4  
; OTHER INFORMATION: (IgE)  
; US-09-847-208-7

Query Match 100.0%; Score 1260; DB 10; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCPCPAPELGGPSVFLPPRKPKDTLMISRTPETCVVWVDSHEDPEVK 60  
Db 1 EPKSCDKTHCPCPAPELGGPSVFLPPRKPKDTLMISRTPETCVVWVDSHEDPEVK 60  
QY 61 NWYDVGVEVHNVKTKPREEQYNSTRVWSVLTVHQNMNGKEYKCKVSNKALPIEKT 120  
Db 61 NWYDVGVEVHNVKTKPREEQYNSTRVWSVLTVHQNMNGKEYKCKVSNKALPIEKT 120  
QY 121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
QY 181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232  
Db 181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232

RESULT 6  
US-10-000-439-7  
; Sequence 7, Application US/10000439  
; Publication No. US2003006463A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000, 439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847, 208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PastSEQ For Windows Version 4.0  
; SEQ ID NO: 7  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3  
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence  
; US-10-000-439-7

Query Match 100.0%; Score 1260; DB 14; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCPCPAPELGGPSVFLPPRKPKDTLMISRTPETCVVWVDSHEDPEVK 60  
Db 1 EPKSCDKTHCPCPAPELGGPSVFLPPRKPKDTLMISRTPETCVVWVDSHEDPEVK 60  
QY 61 NWYDVGVEVHNVKTKPREEQYNSTRVWSVLTVHQNMNGKEYKCKVSNKALPIEKT 120  
Db 61 NWYDVGVEVHNVKTKPREEQYNSTRVWSVLTVHQNMNGKEYKCKVSNKALPIEKT 120  
QY 121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
QY 181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232  
Db 181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232

RESULT 7  
US-09-996-357-10  
; Sequence 10, Application US/09996357  
; Patent No. US200133001A1  
; GENERAL INFORMATION:  
; APPLICANT: Gefter, Malcolm L  
; APPLICANT: Israel, David I  
; APPLICANT: Joyal, John L  
; APPLICANT: Gosselin, Michael  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
; TREATING AN AMYLOIDOCENIC DISEASE  
; FILE REFERENCE: PPI-105  
; CURRENT APPLICATION NUMBER: US/09/996, 357  
; CURRENT FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 60/253, 302  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/250, 198  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/257, 186  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 10  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-996-357-10

Query Match 97.2%; Score 1225; DB 9; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCPCPAPELGGPSVFLPPRKPKDTLMISRTPETCVVWVDSHEDPEVK 60  
Db 1 EPKSCDKTHCPCPAPELGGPSVFLPPRKPKDTLMISRTPETCVVWVDSHEDPEVK 60  
QY 61 NWYDVGVEVHNVKTKPREEQYNSTRVWSVLTVHQNMNGKEYKCKVSNKALPIEKT 120  
Db 61 NWYDVGVEVHNVKTKPREEQYNSTRVWSVLTVHQNMNGKEYKCKVSNKALPIEKT 120  
QY 121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
Db 121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
QY 181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232  
Db 181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232

RESULT 8  
US-09-389-782-1  
; Sequence 1, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Woden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389, 782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-389-782-1

121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
121 ISKAKVQPREPVYVTLPPSDELTKNQVSITCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
181 PVLDVGSEFLYSKLTVDKSRWQQNVFSCSVMHALHNHYTOKSLSLSPGK 232

Query Match 97.2%; Score 1225; DB 10; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCPAPELIGGSPVLFPPKPDKTLMISRTPETVCVVDVSHDPEVKF 60  
 Db 1 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 120  
 Qy 61 NWYDGVEVNWKPKREQYNSTRVSVLTVLHQNMKGKECKVSKNKAALPIKT 120  
 Db 61 NWYDGVEVNWKPKREQYNSTRVSVLTVLHQDWLNGKEYCKVSKNKAALPIKT 120  
 Qy 121 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Db 121 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Qy 181 PVLDVGSGFLFLYSKLTVDKSRWQGNVFSCSVMEHALHNHYQOSLSLSPKG 232  
 Db 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEHALHNHYQOSLSLSPKG 232

RESULT 9  
 US-10-671-619-7  
 ; Sequence 7 Application US/10617619  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bjorn, Soren E  
 ; APPLICANT: Nicolaisen, Else M  
 ; APPLICANT: Jorgensen, Anker S  
 ; TITLE OF INVENTION: TF Binding Compound  
 ; FILE REFERENCE: 6455\_200-US  
 ; CURRENT APPLICATION NUMBER: US/10/617,619  
 ; CURRENT FILING DATE: 2003-07-11  
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099  
 ; PRIOR FILING DATE: 2002-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/404,568  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 7  
 ; LENGTH: 232  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-10-671-619-7

Query Match 97.2%; Score 1225; DB 16; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCPAPELIGGSPVLFPPKPDKTLMISRTPETVCVVDVSHDPEVKF 60  
 Db 1 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 120  
 Qy 61 NWYDGVEVNWKPKREQYNSTRVSVLTVLHQDWLNGKEYCKVSKNKAALPIKT 120  
 Db 61 NWYDGVEVNWKPKREQYNSTRVSVLTVLHQDWLNGKEYCKVSKNKAALPIKT 120  
 Qy 121 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Db 121 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Qy 181 PVLDVGSGFLFLYSKLTVDKSRWQGNVFSCSVMEHALHNHYQOSLSLSPKG 232  
 Db 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEHALHNHYQOSLSLSPKG 232

RESULT 11  
 US-10-831-622-97  
 ; Sequence 97 Application US/10831622  
 ; Publication No. US2004024825A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaye, Jonathan  
 ; APPLICANT: Wilkinson, Beverley  
 ; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE  
 ; FILE REFERENCE: ISRI 810.1  
 ; CURRENT APPLICATION NUMBER: US/10/831,622  
 ; CURRENT FILING DATE: 2004-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/467,206  
 ; PRIOR FILING DATE: 2003-04-30  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 97  
 ; LENGTH: 232  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-831-622-97

Query Match 97.2%; Score 1225; DB 16; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCPAPELIGGSPVLFPPKPDKTLMISRTPETVCVVDVSHDPEVKF 60  
 Db 1 EPKSCDKTHCPCPAPELIGGSPVLFPPKPDKTLMISRTPETVCVVDVSHDPEVKF 60  
 Qy 61 NWYDGVEVNWKPKREQYNSTRVSVLTVLHQNMKGKECKVSKNKAALPIKT 120  
 Db 61 NWYDGVEVNWKPKREQYNSTRVSVLTVLHQDWLNGKEYCKVSKNKAALPIKT 120  
 Qy 121 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Db 121 ISKAKQPRPQVTLPPSRDELTKNQSLTCLVKGFYPSDIAVEWESNGOPENNYKTP 180  
 Qy 181 PVLDVGSGFLFLYSKLTVDKSRWQGNVFSCSVMEHALHNHYQOSLSLSPKG 232  
 Db 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEHALHNHYQOSLSLSPKG 232

RESULT 10  
 US-10-661-593A-26  
 ; Sequence 26 Application US/10761593A  
 ; Publication No. US20040175824A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sun, Lee-Hwei K  
 ; APPLICANT: Sun, Bill N

Qy 181 PVLDVGSGFLYSLKUTVDKSRWQGQNVFSCSVVMHEALTHNHYQORSLSLSPGK 232  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||  
; Sequence 26, Application US/10800497  
; Publication No. US20040259209A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor with increased biological activities  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUM2001  
; CURRENT APPLICATION NUMBER: US/10/800,497  
; CURRENT FILING DATE: 2004-03-15  
; PRIORITY APPLICATION NUMBER: US/09/968,362  
; PRIORITY FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-10-800-497-26

RESULT 12  
; Sequence 26, Application US/10800497  
; Publication No. US20040259209A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor with increased biological activities  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUM2001  
; CURRENT APPLICATION NUMBER: US/10/800,497  
; CURRENT FILING DATE: 2004-03-15  
; PRIORITY APPLICATION NUMBER: US/09/968,362  
; PRIORITY FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-10-800-497-26

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCAPELGGPSVLFPPKPKDTLMISRTPETCVWVWDVSHEDEPVKF 60  
Db ||||| ||||| ||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||  
; Sequence 208, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390059\_401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 208  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide  
US-10-207-655-208

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCAPELGGPSVLFPPKPKDTLMISRTPETCVWVWDVSHEDEPVKF 60  
Db ||||| ||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||  
; Sequence 13, Application US/10800449  
; Publication No. US20040265973A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Cecily R  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor with increased biological activities  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUM2001  
; CURRENT APPLICATION NUMBER: US/10/800,449  
; CURRENT FILING DATE: 2004-03-15  
; PRIORITY APPLICATION NUMBER: US/09/968,362  
; PRIORITY FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-10-800-449-26

RESULT 14  
; Sequence 208, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390059\_401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 208  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide  
US-10-207-655-208

Query Match 97.2%; Score 1225; DB 14; Length 235;  
Best Local Similarity 97.0%; Pred. No. 6.2e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCAPELGGPSVLFPPKPKDTLMISRTPETCVWVWDVSHEDEPVKF 60  
Db ||||| ||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||  
; Sequence 13, Application US/10800449  
; Publication No. US20040265973A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Cecily R  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor with increased biological activities  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUM2001  
; CURRENT APPLICATION NUMBER: US/10/800,449  
; CURRENT FILING DATE: 2004-03-15  
; PRIORITY APPLICATION NUMBER: US/09/968,362  
; PRIORITY FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-10-800-449-26

RESULT 15  
; Sequence 13, Application US/0996357  
; Publication No. US2002013301A1  
; GENERAL INFORMATION:  
; APPLICANT: Gefter, Malcolm L  
; APPLICANT: Israel, David I  
; APPLICANT: Joyal, John L  
; APPLICANT: Gosselin, Michael

; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
 ; TREATING AN AMYLOIDGENIC DISEASE  
 ; FILE REFERENCE: PPI-105  
 ; CURRENT APPLICATION NUMBER: US/09/396,357  
 ; CURRENT FILING DATE: 2001-11-27  
 ; PRIOR APPLICATION NUMBER: 60/253,302  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/250,198  
 ; PRIOR FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: 60/257,186  
 ; PRIOR FILING DATE: 2000-12-20  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 13  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-396-357-13

Query Match 97 %; Score 1225; DB 9; Length 247;  
 Best Local Similarity 97.0%; Pred. No. 6.6e-90; Mismatches 4; Indels 0; Gaps 0;  
 Matches 225; Conservative 3;

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QY  1 EPKSCDKTHICPPCAPELLGGPSVPLFPKPDKTLMISRTPWTCVVVDYSHDPEVKP 60
Db  16 EPKSCDKTHICPPCAPELLGGPSVPLFPKPDKTLMISRTPWTCVVVDYSHDPEVKP 75
QY  61 NWYVPGVEVANVKTKPREEQNSTMTRVSVLTVLUNQWMNGKEYKCKVSNKALPPIKT 120
Db  76 NWYVPGVEVANAKTKPREEQNSTMTRVSVLTVLUNQDWLNGKEKCKVSNKALPPIKT 135
QY  121 ISKAKVQPRREQVYLPPSRDELTKNQVSLTCLVKGFYPSDIATEWESNCOPENNYKTP 180
Db  136 ISKAKGQPREQVYLPPSRDELTKNQVSLTCLVKGFYPSDIATEWESNCOPENNYKTP 195
QY  181 PVLDVGSGFLYSLKLTVDSRMRQGNFSSVMHEALHNHQQLSLSLSPK 232
Db  196 PVLDGSFLYSLKLTVDSRMRQGNFSSVMHEALHNHQQLSLSLSPK 247
  
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Search completed: June 7, 2005, 09:25:07  
 Job time : 102.775 secs

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## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 32.456 Seconds  
 (without alignments)  
 533.603 Million cell updates/sec

Title: US-10-000-439-3  
 Perfect score: 1  
 Sequence: 1 EPKSCDKTHCPPCPAPELL.....MHEALHNHYQQRSLISLSPGK 232  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued.PatentsB\_AA:\*

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 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
 5: /cgn2\_6/ptodata/1/1aa/6C\_COMB.pep: \*  
 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result  
No.

Score      Query %  
Match Length DB ID

## Description

RESULT 1 US-08-595-043A-50					
; Sequence 50, Application US/08595043A					
; Patent No. 5935824					
; GENERAL INFORMATION:					
; APPLICANT: SGARLATO, GREGORY D.					
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM					
; NUMBER OF SEQUENCES: 90					
; CORRESPONDENCE ADDRESS:					
; ADDRESSE: MEDLINE & CARROLL					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
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; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					
; STATE: CALIFORNIA					
; COUNTRY: UNITED STATES OF AMERICA					
; ZIP: 94104					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/595, 043A					
; FILING DATE: 31-JAN-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: CARROLL, PETER G.					
; REGISTRATION NUMBER: 32,817					
; REFERENCE/DOCKET NUMBER: SGAR-00371					
; TELECOMMUNICATION INFORMATION:					
; STREET: 220 MONTGOMERY STREET, SUITE 2200					
; CITY: SAN FRANCISCO					

Query Match 97.2%; Score 1225; DB 3; Length 331;  
 Best Local Similarity 97.0%; Pred. No. 6.1e-116; Indels 0;  
 Matches 225; Conservative 3; Mismatches 4; Gaps 0;

Qy 1 1 EPKSCDKTHTCPPAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 60  
 Db 100 EPKSCDKTHTCPPAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 159

Qy 181 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 232  
 Db 181 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 232

RESULT 2  
 US-09-988-362A-26  
 Sequence 26, Application US/09968362A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sun, Lee-Hwei K  
 ; APPLICANT: Sun, Bill  
 ; APPLICANT: Sun, Cecily R  
 ; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
 ; FILE REFERENCE: 0350201  
 ; CURRENT APPLICATION NUMBER: US/09/968,362A  
 ; CURRENT FILING DATE: 2001-10-01  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 26  
 ; LENGTH: 232  
 ; TYPE: PRT  
 ; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
 ; US-09-988-362A-26

Query Match 97.2%; Score 1225; DB 4; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 3.6e-116; Indels 0; Gaps 0;  
 Matches 225; Conservative 3; Mismatches 4; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 60  
 Db 1 EPKSCDKTHTCPPCAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 60

Qy 61 NWYVGDGVENAVKVKPREEQNSTMTRVSVLTVLHQDNMNGKEYCKVSKNSKALPAIET 120  
 Db 61 NWYVGDGVENAVKVKPREEQNSTMTRVSVLTVLHQDNMNGKEYCKVSKNSKALPAIET 120

Qy 121 ISKAQVQPREQVYLPPSRDELTKNQVSITCLVKGYPSDIATEWESNGOPENNYKTP 180  
 Db 121 ISKAQVQPREQVYLPPSRDELTKNQVSITCLVKGYPSDIATEWESNGOPENNYKTP 180

Qy 181 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 232  
 Db 181 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 232

RESULT 3  
 US-09-178-869-2  
 Sequence 2, Application US/09178869B  
 ; Patient No. 619794  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tao, Weng  
 ; APPLICANT: Wong, Shou  
 ; APPLICANT: Hickey, William F  
 ; APPLICANT: Hammang, Joseph P.  
 ; APPLICANT: Baetge, E. Edward  
 ; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
 ; FILE REFERENCE: 17810-043  
 ; CURRENT APPLICATION NUMBER: US/09/761,413  
 ; PRIORITY FILING DATE: 1998-10-26  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 331  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-761-413-2

Query Match 97.2%; Score 1225; DB 4; Length 331;  
 Best Local Similarity 97.0%; Pred. No 6.1e-116; Indels 0; Gaps 0;  
 Matches 225; Conservative 3; Mismatches 4; Gaps 0;

Qy 1 EPKSCDKTHTCPPAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 60  
 Db 100 EPKSCDKTHTCPPAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 159

Qy 61 NWYVGDGVENAVKVKPREEQNSTMTRVSVLTVLHQDNMNGKEYCKVSKNSKALPAIET 120  
 Db 160 NWYVGDGVENAVKVKPREEQNSTMTRVSVLTVLHQDNMNGKEYCKVSKNSKALPAIET 219

Qy 121 ISKAQVQPREQVYLPPSRDELTKNQVSITCLVKGYPSDIATEWESNGOPENNYKTP 180  
 Db 220 ISKAQVQPREQVYLPPSRDELTKNQVSITCLVKGYPSDIATEWESNGOPENNYKTP 279

Qy 181 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 232  
 Db 280 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 331

RESULT 4  
 US-09-761-413-2  
 Sequence 2, Application US/09761413  
 ; Patient No. 650691  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tao, Weng  
 ; APPLICANT: Wong, Shou  
 ; APPLICANT: Hickey, William F  
 ; APPLICANT: Hammang, Joseph P.  
 ; APPLICANT: Baetge, E. Edward  
 ; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
 ; FILE REFERENCE: 17810-043  
 ; CURRENT APPLICATION NUMBER: US/09/761,413  
 ; PRIORITY FILING DATE: 1998-10-26  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 331  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-761-413-2

Query Match 97.2%; Score 1225; DB 4; Length 331;  
 Best Local Similarity 97.0%; Pred. No 6.1e-116; Indels 0; Gaps 0;  
 Matches 225; Conservative 3; Mismatches 4; Gaps 0;

Qy 1 EPKSCDKTHTCPPAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 60  
 Db 100 EPKSCDKTHTCPPAPELGGPSVFLPPKPDTLMISRPTPEVTCVVVDVSHBDEPKF 159

Qy 61 NWYVGDGVENAVKVKPREEQNSTMTRVSVLTVLHQDNMNGKEYCKVSKNSKALPAIET 120  
 Db 160 NWYVGDGVENAVKVKPREEQNSTMTRVSVLTVLHQDNMNGKEYCKVSKNSKALPAIET 219

Qy 121 ISKAQVQPREQVYLPPSRDELTKNQVSITCLVKGYPSDIATEWESNGOPENNYKTP 180  
 Db 220 ISKAQVQPREQVYLPPSRDELTKNQVSITCLVKGYPSDIATEWESNGOPENNYKTP 279

Qy 181 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 232  
 Db 280 PVLDVGSEFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 331

RESULT 5  
 US-09-180-100-11  
 Sequence 11, Application US/09180100  
 ; Patient No. 6306395  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAMURA, No. 6306395

US-09-178-869-2

US-09-178-869-2

NUMBER OF SEQ ID NOS: 14, 2, 0  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 331  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-178-869-2

APPLICANT: NAGATA, Shigezau  
 TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
 FILE REFERENCE: 1110-207P  
 CURRENT APPLICATION NUMBER: US/09/180,100  
 CURRENT FILING DATE: 1998-11-02  
 EARLIER APPLICATION NUMBER: PCT/JP97/01502  
 EARLIER FILING DATE: 1997-05-01  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 11  
 LENGTH: 360  
 TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-180-100-11

;

Query Match

Best Local Similarity 97.2%; Score 1225; DB 3; Length 360;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCPPCAPELIGGSVPLFPKPDKTLMISRTPETCVWVVDVSHEDPEVKF 60

Db 129 EPKSCDKTHCPPCAPELIGGSVPLFPKPDKTLMISRTPETCVWVVDVSHDEPVKF 183

QY 61 NWYVGVEVIRNKTKPREEQYNSTRVSVLTVLQINWMNGKEYKCKVSNAKALAPIKT 120

Db 189 NWYVGVEVIRNKTKPREEQYNSTRVSVLTVLQINWMNGKEYKCKVSNAKALAPIKT 248

QY 121 ISAKWQPRQQVYLPPSDDELTKNQVSITCLVKGFYPSDIAYEWESNGOPENNYKTP 180

Db 249 ISAKWQPRQQVYLPPSDDELTKNQVSITCLVKGFYPSDIAYEWESNGOPENNYKTP 303

QY 181 PVLDVGSPFLYSLKLTVDKSRWQGQNVFSCSVMHEALTHNHYQOKSLSLSPGK 232

Db 309 PVLDSDGSFLYSLKLTVDKSRWQGQNVFSCSVMHEALTHNHYQOKSLSLSPGK 360

RESULT 6

US-08-236-311-7

;

Sequence 7, Application US/08236311

;

Patent No. 5565335

;

GENERAL INFORMATION:

;

APPLICANT: Gregory, Timothy J.

;

TITLE OF INVENTION: Adheson Variants

;

NUMBER OF SEQUENCES: 25

;

CORRESPONDENCE ADDRESS:

;

ADDRESSEE: Genentech, Inc.

;

STREET: 460 Point San Bruno Blvd

;

CITY: South San Francisco

;

STATE: California

;

COUNTRY: USA

;

ZIP: 94080

;

COMPUTER READABLE FORM:

;

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

;

COMPUTER: IBM PC compatible

;

OPERATING SYSTEM: PC-DOS/MS-DOS

;

SOFTWARE: Patin (Genentech)

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/08/236,311

;

FILING DATE: 02-MAY-1994

;

CLASSIFICATION: 435

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/936190

;

FILING DATE: 26-AUG-1992

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/842777

;

FILING DATE: 18-FEB-1992

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/250785

;

FILING DATE: 28-SEP-1988

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/104329

;

FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 444P1C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 371 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-236-311-7

;

Query Match

Best Local Similarity 97.0%; Pred. No. 7.2e-116; Length 371;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCPPCAPELIGGSVPLFPKPDKTLMISRTPETCVWVVDVSHEDPEVKF 60

Db 140 EPKSCDKTHCPPCAPELIGGSVPLFPKPDKTLMISRTPETCVWVVDVSHEDPEVKF 199

QY 61 NWYVGVEVIRNKTKPREEQYNSTRVSVLTVLQINWMNGKEYKCKVSNAKALAPIKT 120

Db 200 NWYVGVEVIRNKTKPREEQYNSTRVSVLTVLQINWMNGKEYKCKVSNAKALAPIKT 259

QY 121 ISAKWQPRQQVYLPPSDDELTKNQVSITCLVKGFYPSDIAYEWESNGOPENNYKTP 180

Db 260 ISAKWQPRQQVYLPPSDDELTKNQVSITCLVKGFYPSDIAYEWESNGOPENNYKTP 319

QY 181 PVLDVGSPFLYSLKLTVDKSRWQGQNVFSCSVMHEALTHNHYQOKSLSLSPGK 232

Db 320 PVLDSDGSFLYSLKLTVDKSRWQGQNVFSCSVMHEALTHNHYQOKSLSLSPGK 371

;

RESULT 7

US-08-457-918-7

;

Sequence 7, Application US/08457918

;

Patent No. 6117655

;

GENERAL INFORMATION:

;

APPLICANT: Capon, Daniel J.

;

TITLE OF INVENTION: Adheson Variants

;

NUMBER OF SEQUENCES: 25

;

CORRESPONDENCE ADDRESS:

;

ADDRESSEE: Genentech, Inc.

;

STREET: 460 Point San Bruno Blvd

;

CITY: South San Francisco

;

STATE: California

;

COUNTRY: USA

;

ZIP: 94080

;

COMPUTER READABLE FORM:

;

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

;

COMPUTER: IBM PC compatible

;

OPERATING SYSTEM: PC-DOS/MS-DOS

;

SOFTWARE: Patin (Genentech)

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/08/457,918

;

FILING DATE: 02-MAY-1995

;

CLASSIFICATION: 435

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 08/236311

;

FILING DATE: 02-MAY-1994

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/842777

;

FILING DATE: 26-AUG-1992

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/936190

;

FILING DATE: 26-AUG-1990

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/250785

;

FILING DATE: 28-SEP-1988

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 07/104329

;

FILING DATE: 02-OCT-1987

;

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/104329  
 FILING DATE: 02-OCT-1987  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kubinec, Jeffrey S.  
 REGISTRATION NUMBER: 36,575  
 REFERENCE/DOCKET NUMBER: P0444P1C3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-8228  
 TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 371 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-417-918-7

RESULT 8

Query Match 97.2%; Score 1225; DB 3; Length 371;  
 Best Local Similarity 97.0%; Pred. No. 7.2e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKTLMISRTPETCVVWVDVSHDPEVKF 60  
 Db 140 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKTLMISRTPETCVVWVDVSHDPEVKF 199  
 Qy 61 NWYVGVEVHNVKTKPREQSYNSTRWSLTVLHONWNGKEYKCKVSKNKAALPPIKT 120  
 Db 200 NWYVGVEVHNVKTKPREQSYNSTRWSLTVLHONWNGKEYKCKVSKNKAALPPIKT 259  
 Qy 121 ISKAKVQPREQVYTLPSPRDELTKNQSLTCUVKGKFYPSDIANEWSNGOPENNYKTP 180  
 Db 260 ISKAKVQPREQVYTLPSPRDELTKNQSLTCUVKGKFYPSDIANEWSNGOPENNYKTP 319  
 Qy 181 PVLDVGSGFFLYSKLTVDKSRWQOGNVSSEVMHEALHNHYQOSLSLSPGK 232  
 Db 320 PVLDVGSGFFLYSKLTVDKSRWQOGNVSSEVMHEALHNHYTOKSLSLSPGK 371

RESULT 9

US-10-157-408-7

Query Match 97.2%; Score 1225; DB 4; Length 371;  
 Best Local Similarity 97.0%; Pred. No. 7.2e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKTLMISRTPETCVVWVDVSHDPEVKF 60  
 Db 140 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKTLMISRTPETCVVWVDVSHDPEVKF 199  
 Qy 61 NWYVGVEVHNVKTKPREQSYNSTRWSLTVLHONWNGKEYKCKVSKNKAALPPIKT 120  
 Db 200 NWYVGVEVHNVKTKPREQSYNSTRWSLTVLHONWNGKEYKCKVSKNKAALPPIKT 259  
 Qy 121 ISKAKVQPREQVYTLPSPRDELTKNQSLTCUVKGKFYPSDIANEWSNGOPENNYKTP 180  
 Db 260 ISKAKVQPREQVYTLPSPRDELTKNQSLTCUVKGKFYPSDIANEWSNGOPENNYKTP 319  
 Qy 181 PVLDVGSGFFLYSKLTVDKSRWQOGNVSSEVMHEALHNHYQOSLSLSPGK 232  
 Db 320 PVLDVGSGFFLYSKLTVDKSRWQOGNVSSEVMHEALHNHYTOKSLSLSPGK 371

RESULT 9

US-09-180-100-22

Query Match 97.2%; Score 1225; DB 3; Length 376;  
 Best Local Similarity 97.0%; Pred. No. 7.3e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKTLMISRTPETCVVWVDVSHDPEVKF 60  
 Db 145 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKTLMISRTPETCVVWVDVSHDPEVKF 204  
 Qy 61 NWYVGVEVHNVKTKPREQSYNSTRWSLTVLHONWNGKEYKCKVSKNKAALPPIKT 120  
 Db 205 NWYVGVEVHNVKTKPREQSYNSTRWSLTVLHONWNGKEYKCKVSKNKAALPPIKT 264

RESULT 10  
US-08-784-512-3  
; Sequence 3, Application US/08784512  
; Patent No. 5872209  
GENERAL INFORMATION:  
APPLICANT: BARTNIK, Eckart  
APPLICANT: BEIDENMUELLER, Bernd  
APPLICANT: BUETTNER, Frank  
APPLICANT: CATERSON, Bruce  
APPLICANT: HUGHES, Clare  
TITLE OF INVENTION: An artificial recombinant substrate (RAGG 1)  
TITLE OF INVENTION: and native aggrecan to study the proteolytic activity of  
TITLE OF INVENTION: "Aggrecanase" in cell culture systems  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,512  
FILING DATE: 17-JAN-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 96100682.2  
FILING DATE: 18-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/311  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..396  
US-08-784-512-3

Query Match 97.2%; Score 1225; DB 2; Length 396;  
Best Local Similarity 97.0%; Pred. No. 7.9e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCCPAPELGGPSVILFPPKPKDTLMISRPTPEVTCVVVDVSHEDPEVKF 60  
Db 165 EPKSCDKTHCPCCPAPELGGPSVLFPPKPKDTLMISRPTPEVTCVVVDVSHEDPEVKF 224  
Qy 61 NWYDGVENVHAKTKPREEQNSTYRVSVLVLQHNMWNGKEYKCKVSKNKLAPIEKT 120  
Db 225 NWYDGVENVHAKTKPREEQNSTYRVSVLVLQHNMWNGKEYKCKVSKNKLAPIEKT 284

RESULT 11  
US-09-176-228-3  
; Sequence 3, Application US/09176228  
; Patent No. 6180334  
GENERAL INFORMATION:  
APPLICANT: BARTNIK, Eckart  
APPLICANT: BEIDENMUELLER, Bernd  
APPLICANT: BUETTNER, Frank  
APPLICANT: CATERSON, Bruce  
APPLICANT: HUGHES, Clare  
TITLE OF INVENTION: An artificial recombinant substrate (RAGG 1)  
TITLE OF INVENTION: and native aggrecan to study the proteolytic activity of  
TITLE OF INVENTION: "Aggrecanase" in cell culture systems  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/176-228  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,512  
FILING DATE: 17-JAN-1997  
APPLICATION NUMBER: EP 96100682.2  
FILING DATE: 18-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/311  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..396  
US-09-176-228-3

Query Match 97.2%; Score 1225; DB 3; Length 396;  
Best Local Similarity 97.0%; Pred. No. 7.9e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCCPAPELGGPSVLFPPKPKDTLMISRPTPEVTCVVVDVSHEDPEVKF 60  
Db 165 EPKSCDKTHCPCCPAPELGGPSVLFPPKPKDTLMISRPTPEVTCVVVDVSHEDPEVKF 224  
Qy 61 NWYDGVENVHAKTKPREEQNSTYRVSVLVLQHNMWNGKEYKCKVSKNKLAPIEKT 120  
Db 225 NWYDGVENVHAKTKPREEQNSTYRVSVLVLQHNMWNGKEYKCKVSKNKLAPIEKT 284

RESULT 12  
PCT-US 95-03866-12

Sequence 12, Application PC/TUS9503866

GENERAL INFORMATION:

APPLICANT: Cytomed, Inc. (all states except US)  
APPLICANT: Nocka, Karl (US only)

APPLICANT: Lobell, Robert B (US only)

TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND NUMBER OF SEQUENCES: FLK-3/FLK-2 LIGAND 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03866

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/220,379  
FILING DATE: 28-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F  
REGISTRATION NUMBER: 27,794

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/220,379  
FILING DATE: 28-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F  
REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: Cytomed/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 424 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

PCT-US95-03866-12

Query Match 97.2%; Score 1225; DB 5; Length 424;  
Best Local Similarity 97.0%; Pred. No. 8.7e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHICPPCPAPELGGPSVLFPPKPKDTLMISRPEVTCVVVDVSHDPEVKF 60  
Db 193 EPKSCDKTHICPPCPAPELGGPSVLFPPKPKDTLMISRPEVTCVVVDVSHDPEVKF 252

Qy 61 NWYVGVEENVKKPREQYNSTRVSVLTVHQWNGKEYKCKVSKNKAPEKT 120  
Db 253 NWYVGVEENVKKPREQYNSTRVSVLTVHQWNGKEYKCKVSKNKAPEKT 312

Qy 121 ISKAKVQPRQVTLPSPRDELTKNOVSITCLVKGFYPSDIATEWESENQOPENNYKTP 180  
Db 313 ISKAKQPRQVTLPSPRDELTKNOVSITCLVKGFYPSDIATEWESENQOPENNYKTP 372

Qy 181 PVLSVGSFELYSKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSLSPGK 232  
Db 373 PVLDSDGSFELYSKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSLSPGK 424

RESULT 13  
PCT-US 95-03866-14

Sequence 14, Application PC/TUS9503866

GENERAL INFORMATION:

APPLICANT: Cytomed, Inc. (all states except US)  
APPLICANT: Nocka, Karl (US only)

APPLICANT: Lobell, Robert B (US only)

TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND NUMBER OF SEQUENCES: FLK-3/FLK-2 LIGAND 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03866

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/220,379  
FILING DATE: 28-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F  
REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: Cytomed/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 424 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

PCT-US95-03866-14

Query Match 97.2%; Score 1225; DB 5; Length 424;  
Best Local Similarity 97.0%; Pred. No. 8.7e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHICPPCPAPELGGPSVLFPPKPKDTLMISRPEVTCVVVDVSHDPEVKF 60  
Db 193 EPKSCDKTHICPPCPAPELGGPSVLFPPKPKDTLMISRPEVTCVVVDVSHDPEVKF 252

Qy 61 NWYVGVEENVKKPREQYNSTRVSVLTVHQWNGKEYKCKVSKNKAPEKT 120  
Db 253 NWYVGVEENVKKPREQYNSTRVSVLTVHQWNGKEYKCKVSKNKAPEKT 312

Qy 121 ISKAKVQPRQVTLPSPRDELTKNOVSITCLVKGFYPSDIATEWESENQOPENNYKTP 180  
Db 313 ISKAKQPRQVTLPSPRDELTKNOVSITCLVKGFYPSDIATEWESENQOPENNYKTP 372

Qy 181 PVLSVGSFELYSKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSLSPGK 232  
Db 373 PVLDSDGSFELYSKLTVDKSRWQGNVFSCSVMHEALHNHYTOKSLSPGK 424

RESULT 14  
PCT-US 96-10043-11

Sequence 11, Application PC/TUS9610043

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation  
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES

TITLE OF INVENTION: AND METHODS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/10043  
 FILING DATE:  
 CLASSIFICATION:  
 NAME: Lech, Karen F.

PRIOR APPLICATION NUMBER:  
 APPLICATION NUMBER: US 60/000,213  
 TELECOMMUNICATION INFORMATION:  
 FILING DATE: 14-JUN-1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eibing, Karen L.

REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: 00786/284001  
 TELEPHONE: 617/542-5070  
 TELEX: 20154

INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 437 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US96-10043-11

Query Match 97.2%; Score 1225; DB 5; Length 437;  
 Best Local Similarity 97.0%; Pred. No. 9.1e-116;  
 Matches 225; Conservative 3; MisMatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCPAPELGGPSVLFPPKPKDTLMISRPTPEVTVWVDVSHEDPEVKF 60  
 Db 206 EPKSCDKTHCPPCPAPELGGPSVLFPPKPKDTLMISRPTPEVTVWWDVSHEDPEVKF 265

Qy 61 NWYVGVEVANKTKTAKREEQNINSTRVWSVTIVLHQNWMGKEYKKVSKNKLAPIEKT 120  
 Db 266 NWYVGVEVANKTKTAKREEQNINSTRVWSVTIVLHQDWINGKEYKCKVSKNKLAPIEKT 325

Qy 121 ISKAKVQPRPQQVYLPPSDELTKNOVSITCLVKGFYSDIAVWESENQOPENNYKTP 180  
 Db 326 ISKAKVQPRPQQVYLPPSDELTKNOVSITCLVKGFYSDIAVWESENQOPENNYKTP 385

Qy 181 PVLDVGSPFLYSKLTVDKSRWQGNVFSCSVVMHEALHNHYQQRSLSLSPGK 232  
 Db 386 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVVMHEALHNHYTOKSLSLSPGK 437

RESULT 15  
 US-08-472-888A-7  
 ; Sequence 7, Application US/08472888A  
 ; Patent No. 6613746  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Seid, Brian  
 ; APPLICANT: Walz, Gerd  
 ; TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS  
 ; TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Clark & Eibing LLP  
 ; STREET: 176 Federal Street

CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/472,888A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/618,314  
 FILING DATE: 23-NOV-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eibing, Karen L.

REGISTRATION NUMBER: 35,238  
 REFERENCE/DOCKET NUMBER: 00786/258001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-428-0200  
 TELEX: 617-428-7045

INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 442 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-472-888A-7

Query Match 97.2%; Score 1225; DB 4; Length 442;  
 Best Local Similarity 97.0%; Pred. No. 9.3e-116;  
 Matches 225; Conservative 3; MisMatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPPCPAPELGGPSVLFPPKPKDTLMISRPTPEVTVWVDVSHEDPEVKF 60  
 Db 211 EPKSCDKTHCPPCPAPELGGPSVLFPPKPKDTLMISRPTPEVTVWWDVSHEDPEVKF 270

Qy 61 NWYVGVEVANKTKTAKREEQNINSTRVWSVTIVLHQNWMGKEYKKVSKNKLAPIEKT 120  
 Db 271 NWYVGVEVANKTKTAKREEQNINSTRVWSVTIVLHQDWINGKEYKCKVSKNKLAPIEKT 330

Qy 121 ISKAKVQPRPQQVYLPPSDELTKNOVSITCLVKGFYSDIAVWESENQOPENNYKTP 180  
 Db 331 ISKAKVQPRPQQVYLPPSDELTKNOVSITCLVKGFYSDIAVWESENQOPENNYKTP 390

Qy 181 PVLDVGSPFLYSKLTVDKSRWQGNVFSCSVVMHEALHNHYQQRSLSLSPGK 232  
 Db 391 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVVMHEALHNHYTOKSLSLSPGK 442

Search completed: June 7, 2005, 09:04:01  
 Job time : 33.456 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 1.79102 Seconds  
 (without alignment)  
 913.271 Million cell updates/sec

Title: US-10-000-439-13  
 Perfect score: 94

Sequence: 1 ENPVVHFKNIVTPRTP 17

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:  
 1: pir1:  
 2: pir2:  
 3: pir3:  
 4: pir4:  
 SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**ALIGNMENTS**

No.	Score	Query	Match Length	DB ID	Description
1	94	100.0	128	1 MBRTS	myelin basic protein
2	94	100.0	167	2 A37246	myelin basic protein
3	94	100.0	169	1 MBBOB	myelin basic protein
4	94	100.0	171	1 MBC2B	myelin basic protein
5	94	100.0	171	1 MBPGB	myelin basic protein
6	94	100.0	197	1 MBHTB	myelin basic protein
7	94	100.0	328	1 MBMSB	goll-myelin basic protein
8	87	92.6	174	2 S08535	myelin basic protein
9	80	63.8	128	2 S08535	myelin basic protein
10	53	56.4	155	2 B32999	myelin basic protein
11	45	47.9	308	2 G64440	hypothetical protein
12	44	46.8	329	2 R72222	beta-tectorin precursor
13	44	46.8	639	2 T46577	arylsulfatase (EC
14	43	45.7	14	2 S12904	protein kinase (EC
15	43	45.7	85	2 C89965	conserved hypothetical protein
16	43	45.7	134	2 T28704	conserved hypothetical protein
17	43	45.7	395	2 R72222	conserved hypothetical protein
18	43	45.7	672	2 A11183	transcription regulator
19	43	45.7	1124	2 B84742	probable receptor-
20	42	44.7	435	2 AB3076	glutamine synthetase
21	42	44.7	435	2 G98210	glutamate synthetase
22	42	44.7	435	2 JCI301	similar to transcr
23	42	44.7	672	2 AG1541	transcriptional serin
24	42	44.7	672	2 T40137	hypothetical protein
25	41	43.6	48	2 D82534	C;Superfamily: myelin basic protein
26	41	43.6	332	2 B70384	C;Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy
27	41	43.6	480	2 A12308	F;2-128/Product: myelin basic protein S #status experimental #MAT>
28	41	43.6	646	2 A11174	F;2-Modified site: blocked amino end (ala) (in mature form) (probably acetylated) #status F;105/Modified site: omega-N-methylarginine or omega-N-dimethylarginine (Arg) (F
29	41	43.6	690	2 B84945	Omega-N-methylarginine or omega-N-dimethylarginine (Arg) (F)

**RESULT 1**

No.	Score	Query	Match Length	DB ID	Description
1	94	100.0	128	1 MBRTS	myelin basic protein S - rat
					N;Alternate names: small myelin basic protein
					C;Species: Rattus norvegicus (Norway rat)
					C;Date: 24-Apr-1984 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
					C;Accession: B4351; A90275; A94233; A21062; A03142
					R;Schaich, M.; Budoff, R.M.; Stoffel, W.
					Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
					A;Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the t
					A;Reference number: A24351; MUID:87026249; PMID:2429678
					A;Accession: B4351
					A;Molecule type: mRNA
					A;Residues: 1-128 <SCH>
					A;Cross-references: UNIPROT:PO2688; EMBL:M25889; NID:9205321; PIDN:AA41575.1; PID:G20531
					R;Dunkley, P.R.; Carnegie, P.R.
					Biochem. J. 141, 243-255, 1974
					A;Title: Amino acid sequence of the smaller basic protein from rat brain myelin.
					A;Reference number: A90275; MUID:5127359; PMID:4141893
					A;Accession: A90275
					A;Molecule type: protein
					A;Residues: 2-128 <DN>
					A;Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in the
					R;McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McNeally, S.; Shapira, R.
					Science 179, 478-480, 1973
					A;Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogenic
					A;Reference number: A94243; MUID:73180720; PMID:4122324
					A;Accession: A94243
					A;Molecule type: protein
					A;Residues: 46-86 <MC>
					A;Note: the sequence reported for this encephalitogenic peptide differs from that shown by R;Roch, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
					Cell 34, 799-806, 1983
					A;Title: Characterization of cloned cDNA representing rat myelin basic protein: absence of a poly-A tail
					A;Reference number: A21062; MUID:84026484; PMID:6194809
					A;Accession: A21062
					A;Molecule type: mRNA
					A;Residues: 1-124, T, 126-128 <ROA>
					A;Experimental source: strain Sprague-Dawley
					C;Superfamily: myelin basic protein
					C;Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy
					F;2-128/Product: myelin basic protein S #status experimental #MAT>
					F;2-Modified site: blocked amino end (ala) (in mature form) (probably acetylated) #status F;105/Modified site: omega-N-methylarginine or omega-N-dimethylarginine (Arg) (F

Query Match Score 94; DB 1; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 1e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFKNIVTPRTP 17

|||||

**RESULT 2**

A37246 myelin basic protein - guinea pig  
 N;Alternate name: myelin AI protein  
 C;Species: *Cavia porcellus* (guinea pig)  
 C;Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 09-Jul-2004  
 C;Accession: A37246; C92087; R03140  
 R;Debler, G.E.; Martensen, E.R.; Krutzsch, H.C.; Kies, M.W.  
 J; Neurochem. 43, 100-105, 1984  
 A;Title: Sequence of guinea pig myelin basic protein.  
 A;Reference number: A37246; MUID:84215086; PMID:6202840  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-167 <DEI>  
 A;Cross-references: UNIPROT:P25188  
 R;Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.  
 J; Biol. Chem. 246, 4630-4640, 1971  
 A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin  
 A;Reference number: A92087  
 A;Accession: C92087  
 A;Molecule type: protein  
 A;Residues: 45-87 <SHR>  
 C;Superfamily: myelin basic protein  
 C;Keywords: myelin

Query Match 100.0%; Score 94; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIKVTPRTP 17  
 Db 82 ENPVVHFFKNIKVTPRTP 98

**RESULT 3**

MBOB myelin basic protein - bovine  
 N;Alternate names: myelin AI protein  
 C;Species: *Bos primigenius taurus* (cattle)  
 C;Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 09-Jul-2004  
 C;Accession: A92089; A92160; A92087; S53343; A61641; B61641; A03140  
 R;Eylar, E.H.; Brotoff, S.; Hashim, G.; Caccam, J.; Burnett, P.  
 J; Biol. Chem. 246, 5770-5784, 1971  
 A;Title: Basic AI protein of the myelin membrane. The complete amino acid sequence.  
 A;Reference number: A92089; MUID:72007306; PMID:5096093  
 A;Accession: A92089  
 A;Molecule type: protein  
 A;Residues: 1-'S' 2-169 <EYL>  
 A;Cross-references: UNIPROT:P02687  
 R;Brotoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.  
 J; Biol. Chem. 249, 559-567, 1974  
 A;Title: Specific cleavage of the AI protein from myelin with cathepsin D.  
 A;Reference number: A92160; MUID:74070688; PMID:4129204  
 A;Accession: A92160  
 A;Molecule type: protein  
 A;Residues: 1-169 <BRO>  
 R;Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.  
 J; Biol. Chem. 246, 4630-4640, 1971  
 A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin  
 A;Reference number: A92087  
 A;Accession: A92087  
 A;Molecule type: protein  
 A;Residues: 43-87 <SHR>  
 R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.  
 Biochem. J. 306, 551-555, 1995  
 A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia  
 A;Reference number: S54343; MUID:9519433; PMID:7887910  
 A;Accession: S54343

Query Match 100.0%; Score 94; DB 1; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIKVTPRTP 17  
 Db 83 ENPVVHFFKNIKVTPRTP 99

**RESULT 4**

NBCZB myelin basic protein - chimpanzee (tentative sequence)

N;Alternate names: MBP  
 C;Species: *Pan troglodytes* (chimpanzee)  
 C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
 C;Accession: A03139  
 R;Weissman, F.C.; Thompson, M.; Kalter, S.S.  
 Life Sci. 17, 219-223, 1975  
 A;Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.  
 A;Reference number: A03139; MUID:7600921; PMID:51459  
 A;Accession: A03139  
 A;Molecule type: protein  
 A;Residues: 1-171 <WES>  
 A;Cross-references: UNIPROT:P06905  
 C;Comment: This protein may function in maintaining the proper structure of myelin.  
 C;Superfamily: myelin basic protein  
 C;Keywords: blocked amino end; methylated amino acid; myelin; structural protein  
 P;1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental  
 P;1/Modified site: omega-N-methylarginine or omega-N,omega-N-dimethylarginine (Arg) #  
 P;1/Modified site: omega-N-methyarginine or omega-N,omega-N-dimethylarginine (Arg) {

**RESULT 5**

MBGB  
Myelin basic protein - pig (tentative sequence)  
N;Contains: myelin basic protein amide 14  
C;Species: *Sus scrofa domesticus* (domestic pig)  
C;Date: 19-Apr-1995 #sequence\_revision 26-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: A61640; A36245  
R;Kira, J.; Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.  
J. Neurochem. 44, 134-142, 1985  
A;Title: Amino acid sequence of porcine myelin basic protein.  
A;Reference number: A61640; MUID:85056964; PMID:2578056  
A;Molecule type: protein  
A;Residues: 1-171 <KIR>  
A;Cross-references: UNIPROT:PB1558  
A;Note: Some peptides were ordered by homology  
R;Fukamatsu, K.; Tatemoto, K.  
Biophys. Res. Commun. 172, 1167-1174, 1990  
A;Title: Isolation and characterization of a novel peptide amide from porcine brain.  
A;Reference number: A36245; MUID:91058553; PMID:1700904  
A;Accession: A36245  
A;Molecule type: protein  
A;Residues: 1-14 <TRK>  
A;Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu at position 14  
A;Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic C;Superfamily: myelin basic protein  
C;Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis product; myelin basic protein #status experimental <MAT>  
F;1-14#Product: myelin peptide amide-14 #status experimental <PA12>  
F;1#Modified site: acetylated amino end (Ala) #status experimental (amide in mature form myelin peptide ami-  
F;1#Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide ami-  
F;10#Modified site: omega-N-methylarginine or omega-N-omega-N'-dimethylarginine (Arg)  
  

Query	Match	Best Local Similarity	Score	Pred.	No.	DB	Length				
QY	1 ENPVVHFFKONIVTPRTP 17	100.0%	94	DB	1	171					
Db	83 ENPVVHFFKONIVTPRTP 99										
		Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

**RESULT 6**

MBHB  
Myelin basic protein [validated] - human  
N;Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein pre-  
5'K splice form  
C;Species: Homo sapiens (man)  
C;Date: 18-Dec-1981 #sequence\_revision 25-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: S10482; A9106; A90256; JH0802; A60862; A61420; A33273; I54219; I56  
R;Streicher, R.; Stoffel, W.  
Biol. Chem. Hoppe-Seyler 370, 503-510, 1989  
A;Title: The organization of the human myelin basic protein gene. Comparison with the mouse gene  
A;Reference number: S10482; MUID:89302693; PMID:2472816  
A;Accession: S10482  
A;Statute: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-197 <STR>  
A;Cross-references: UNIPROT:PO2686; EMBL:X1286; NID:934490; PIDN:CAA35179.1; PID:gi1842  
R;Kamholz, J.; De Ferra, F.; Puckett, C.; Iazzarini, R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986  
A;Title: Identification of three forms of human myelin basic protein by cDNA cloning.  
A;Reference number: A94106; MUID:86259714; PMID:2425357  
A;Accession: A94106  
A;Molecule type: mRNA  
A;Residues: 1-59 <KAM>  
A;Cross-references: GB:M13577; NID:9187408; PIDN:AAA59562.1; PID:gi307160  
A;Note: 18.5K splice form  
A;Accession: B94106  
A;Molecule type: mRNA  
A;Residues: 1-197 <KA2>  
  

A;Note:	antibody to the exon 2 encoded sequence detected a 21.5K splice form
A;Note:	a 17.2K splice form is also described
A;Note:	antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K splicing variant
R;Carnegie, P.R.	
J. Biomed. J. 123, 57-67, 1971	
Biochem. J. 259, 86-197 <CAR>	
R;Proost, P.; Van Damme, J.; Opdenakker, G.	
Biochem. Biophys. Res. Commun. 192, 1115-1181, 1993	
A;Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin basic protein	
A;Reference number: JH0802; MUID:93282820; PMID:7685161	
A;Accession: JH0802	
A;Molecule type: protein	
A;Residues: 2-59, 86-197 <PRO>	
A;Experimental source: brain	
R;Scoble, H.A.; Whitaker, J.N.; Biemann, K.	
J. Neurochem. 47, 614-616, 1986	
J. Biol. Chem. 259, 5028-5031, 1984	
A;Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 and 2-45	
A;Reference number: A60862; MUID:86280476; PMID:2426402	
A;Accession: A60862	
A;Molecule type: protein	
A;Residues: 2-45, 117-197 <SCO>	
A;Note: evidence for acetylated amino end	
R;Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.	
J. Biol. Chem. 259, 5028-5031, 1984	
A;Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by sequencing and Edman degradation	
A;Reference number: A6120; MUID:9185608; PMID:201481	
A;Accession: A61420	
A;Molecule type: protein	
A;Residues: 46-59, 80-116 <GIB>	
R;Wood, D.D.; Moscarello, M.A.	
J. Biol. Chem. 264, 5121-5127, 1989	
A;Title: The isolation, characterization, and lipid-aggregating properties of a citrulline-rich peptide from the brain	
A;Reference number: A33273; MUID:89174797; PMID:2466844	
A;Accession: A33273	
A;Molecule type: protein	
A;Residues: 15-25, 'X', 27-31, 'X', 33-59, 86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <WOC>	
A;Note: form C-8, residues designated 'X' were determined as citrulline	
R;Baldwin, G.S.; Carnegie, P.R.	
J. Biol. Chem. 122, 69-74, 1971	
A;Title: Isolation and partial characterization of methylated arginines from the encephalomyelitis protein	
A;Reference number: A90257; MUID:206601; PMID:5128665	
A;Contents: annotation; methylation	
A;Reference number: A90257; MUID:206601; PMID:5128665	
A;Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approxi- mately 17.2K protein	
R;Levitt, V.A.; Wilks, F.; Carnegie, P.R.	
J. Immunol. 105, 1223-1230, 1970	
A;Reference number: A92806; MUID:71088405; PMID:4099924	
A;Contents: annotation	
A;Note: a region including residues 133-149 induces experimental autoimmune encephalomyelitis	
R;Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.	
Genomics 6, 16-22, 1990	
A;Title: Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a new form of repetitive DNA	
A;Reference number: I54219; MUID:90152679; PMID:1689270	
A;Accession: I54219	
A;Status: preliminary; translated from GB/EMBL/DDBJ	
A;Molecule type: DNA	
A;Residues: 1-59 <RE3>	
A;Cross-references: GB:M63599; NID:9187402; PIDN:AAA59560.1; PID:gi187403	
R;Roth, H.J.; Kronquist, K.B.; Kerlero de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.	
J. Neurosci. Res. 17, 321-328, 1987	
A;Title: Evidence for the expression of four myelin basic protein variants in the developing mouse brain	
A;Reference number: I56567; MUID:87311781; PMID:2442403	
A;Accession: I56567	
A;Status: preliminary; translated from GB/EMBL/DDBJ	
A;Molecule type: mRNA	
A;Residues: 1-132, 44-197 <RE3>	
A;Cross-references: GB:M30516; NID:9187410; PIDN:AAA59563.1; PID:gi307161	
A;Accession: I73634	
A;Status: preliminary; translated from GB/EMBL/DDBJ	
A;Molecule type: mRNA	
A;Residues: 1-197 <KA2>	

A;Residues: 1-197 <RE3>  
A;Cross-references: GB:M30515; NID:g187412; PIDN:AAA59564\_1; PID:g307162  
R;Doch, H.J.; Krongauz, K.; Pretorius, P.J.; Crandall, B.R.; Campagnoni, A.T.  
J. Neurosci. Res. 16, 227-238, 1986

A;Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin basic protein precursor - mouse  
A;Reference number: 156565; MUID:86308101; PMID:2427738

A;Accession: 156565  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA

A;Residues: 1-59, 86-133, 145-197 <RE4>  
A;Cross-references: GB:M3047; NID:g187400; PIDN:AAA59559\_1; PID:g307159  
A;Reference number: S66383; MUID:96004793; PMID:7574672

A;Molecule type: protein  
A;Residues: 23-25, X, 27-39 <BOU>  
C;Comment: Four alternatively spliced forms of myelin basic protein have been observed,  
C;Genetics:  
A;Gene: GDB:MBP

A;Cross-references: GDB:119379; OMIM:159430  
A;Map position: 18q22-18qter  
A;Introns: 5/3; 85/3; 120/3; 132/3; 143/3; 183/3  
C;Function:  
A;Description: probably helps maintain myelin structure  
C;Superfamily: myelin basic protein

C;Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimmunity; MBP

F;197-product: myelin basic protein, 21.5K splice form #status predicted <MT1>  
F;197-product: myelin basic protein, 20.2K splice form #status predicted <MT2>  
F;197-product: myelin basic protein, 18.5K splice form #status experimental <MT3>  
F;197-product: myelin basic protein, 17.2K splice form #status predicted <MT4>  
F;2-59, 86-132, 144-197-product: myelin basic protein, 17.2K splice form #status experimental <MT5>  
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F;2/Modified site: citrulline (Arg) (in form C-8) #status experimental  
F;134/Modified site: omega-N-methylarginine or omega-N,omega-N-dimethylarginine (Arg) (in mature form C-8) #status experimental

Query 1 ENPVVHFFKQIVTPRPP 17  
Db 110 ENPVVHFFKQIVTPRPP 126

RESULT 7

MBMB  
Golli-myelin basic protein precursor - mouse  
N;Alternate names: Golli-mbp protein; MBP  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Mar-1987 #sequence change 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: A45421; B4421; A90875; A26591; B26591; A60920; I4807; I58996; I54  
R;Campagnoni, A.T.; Ribi, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry, J.; Biol. Chem. 268, 4930-4938, 1993  
A;Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that encodes a 105-kilodalton myelin basic protein precursor  
A;Reference number: A45421; MUID:93186801; PMID:7680345  
A;Molecule type: mRNA  
A;Accession: A45421  
A;Cross-references: UNIPROT:04370; GB:107507; NID:g193584  
A;Experimental source: clone J37  
A;Note: Sequence extracted from NCBI backbone (NCBIN:126696) and modified  
A;Accession: B45421  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-190; 217-216; 316-328 <CM1>  
A;Cross-references: UNIPROT:04370; GB:107507; NID:g193584  
A;Experimental source: clone J37  
A;Note: Sequence extracted from NCBI backbone (NCBIN:126696) and modified  
A;Accession: B45421  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-191, SSEP, <CM2>  
A;Cross-references: GB:107508; NID:g193586; PIDN:AAA37721\_1; PID:g193587  
A;Experimental source: clone BG21  
A;Note: sequence extracted from NCBI backbone (NCBIN:126700; NCICB:126715)  
R;de Ferra, F.; Eng, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molinleaux, S.; Lazzarini, Cell 43, 721-727, 1985

A;Title: Alternative splicing accounts for the four forms of myelin basic protein.  
A;Reference number: A90875; MUID:86079555; PMID:2416470  
A;Accession: A90875  
A;Molecule type: mRNA

A;Residues: 134-328 <DEF>  
A;Cross-references: GB:100404; GB: M11669; NID:g199060; PIDN:AAA39502\_1; PID:g387414  
A;Title: Cloning and characterization of the myelin basic protein gene from mouse: one gene, two mRNAs  
A;Reference number: A90867; MUID:85254913; PMID:2410136  
A;Accession: A90867  
A;Molecule type: DNA  
A;Residues: 134-190, 217-328 <TAK>  
A;Cross-references: GB:ML153; NID:g199044; PIDN:AAA39496\_1; PID:g387414  
A;Experimental source: 18.5K  
R;Newman, S.; Kitamura, K.; Campagnoni, A.T.  
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987  
A;Title: Identification of a cDNA coding for a fifth form of myelin basic protein in mouse  
A;Reference number: A94188; MUID:87118269; PMID:2433693  
A;Accession: A26591  
A;Molecule type: mRNA  
A;Cross-references: GB:M15060; NID:g199048; PIDN:AAB59711\_1; PID:g199049  
A;Experimental source: clone M722; splice form 17.22K  
A;Accession: B26591  
A;Molecule type: mRNA  
A;Residues: 134-190, 217-263, 275-328 <NEW1>  
A;Cross-references: GB:ML15062; NID:g199050  
A;Experimental source: clone M78; splice form 17.24K  
R;Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.W.; J. Neurochem. 54, 2032-2041, 1990  
A;Title: Expression of a novel transcript of the myelin basic protein gene.  
A;Reference number: A60920; MUID:90250449; PMID:1692584  
A;Accession: A60920  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 134-190, 217-274, 316-328 <KIT>  
A;Experimental source: M41; Splice form 14K  
R;Grima, B.; Zelenika, D.; Pebzac, B.  
J. Neurochem. 59, 2318-2323, 1992  
A;Title: A novel transcript overlapping the myelin basic protein gene.  
A;Reference number: 148407; MUID:93057537; PMID:1279125  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Accession: 148407  
A;Cross-references: EMBL:X67319; NID:g951332; PIDN:CAN47733\_1; PID:g51333  
A;Note: Submitted to the EMBL Data Library, July 1992  
R;Zeller, N.K.; Hunkele, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984  
A;Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin basic protein gene  
A;Reference number: 158996; MUID:84115431; PMID:6198644  
A;Accession: 158996  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 239-248 <ZEP>  
A;Cross-references: GB:00989; NID:g199037; PIDN:AAA39495\_1; PID:g554195  
R;Murata, M.; Tamura, T.  
Gene 75, 31-39, 1999  
A;Title: The promoter elements of the mouse myelin basic protein gene function efficiently  
A;Reference number: 154033; MUID:89252919; PMID:2470651  
A;Cross-references: 154033  
A;Accession: 154033  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 134-157 <MT1>  
A;Cross-references: GB:M24410; NID:g199052; PIDN:AAA39498\_1; PID:g554196  
R;Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Ohshima, M.; Mikoshiba, K.  
EMBO J. 7, 77-83, 1988  
A;Title: Gene organization and transcription of duplicated MBP genes of myelin deficient  
A;Reference number: 153256; MUID:88196094; PMID:2452084  
A;Accession: 153256  
A;Status: translation not shown; translated from GB/EMBL/DBBJ

A;Molecule type: DNA  
A;Residues: 217-229, 'HN', 232-250 <OKA>  
A;Cross-references: GB:36275; NID:919069; PIDN:AAA39504.1; PID:g293725  
A;Note: hypothetical translation of the reversed and complementary sequence to that shown  
C;Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and 16.5K.  
C;Genetics:  
A;Gene: Goli-mbp; shi-mld  
A;Introns: 190/3; 250/3; 262/3; 273/3; 314/3  
C;Function:  
A;Description: probably helps maintain myelin structure  
C;Superfamily: myelin basic protein  
C;Keywords: alternative splicing; myelin; structural protein  
C;KeyWords: myelin basic protein, splice form 21.5K #status predicted <MAT>  
F;1-190,217-276,316-328#product: myelin basic protein, splice form 21.5K #status predicted <MAT>  
F;134-328#product: myelin basic protein, splice form 17K-a #status predicted <MA>  
F;134-190,217-328#product: myelin basic protein, splice form 17K-b #status predicted <MA>  
F;134-190,217-263,275-328#product: myelin basic protein, splice form 17K-b #status predicted <MA>  
F;134-190,217-274,316-328#product: myelin basic protein, splice form 17K #status predicted <MA>  
Query Match 100.0%; Score 94; DB 1; Length 328;  
Best Local Similarity 100.0%; Pred. No. 3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 240 ENPVVHFFKQNIKVTPRP 256

RESULT 8

S08355 myelin basic protein - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 09-Jul-2004  
C;Accession: S08355  
R;Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.  
Glia 2, 241-249, 1989  
A;Title: Developmental accumulation and heterogeneity of myelin basic protein transcript  
A;Reference number: S08355; MUID:89358239; PMID:2475444  
A;Accession: S08355  
A;Molecule type: mRNA  
A;Residues: 1-174 <ZOP>  
A;Cross-references: UNIPROT:P15720; EMBL:X17103; NID:963594; PIDN:CAA34959.1; PID:g63595  
C;Superfamily: myelin basic protein  
Query Match 92.6%; Score 87; DB 2; Length 174;  
Best Local Similarity 88.2%; Pred. No. 2.3e-07;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Db 82 ENPVVHFFKQNIKVTPRP 98

RESULT 9

A60215 myelin basic protein - dusky shark (fragments)  
C;Species: Carcharhinus obscurus (dusky shark)  
C;Date: 10-Nov-1992 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A60215  
R;Mile, T.J.; Atkins, A.R.; Warren, J.A.; Auton, W.P.; Smith, R.  
J. Neurochem. 55, 950-955, 1990  
A;Title: Shark myelin basic protein: amino acid sequence, secondary structure, and self-  
A;Accession: A60215  
A;Molecule type: protein  
A;Residues: 1-128 <ML>  
A;Cross-references: UNIPROT:p98190  
A;Note: the source was designated as Carcharhinus obscurus (whaler shark)  
C;Superfamily: myelin basic protein  
Query Match 63.8%; Score 60; DB 2; Length 128;  
Best Local Similarity 52.9%; Pred. No. 0.0066;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

RESULT 10

B32999 myelin basic protein - horn shark  
C;Species: Heptodon francisci (horn shark)  
C;Date: 21-Feb-1990 #sequence\_revision 21-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: B32999  
R;Savredra, R.A.; Fors, L.; Heberhold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, I.  
J. Mol. Evol. 29, 149-166, 1989  
A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the teleost fish.  
A;Reference number: A32999; MUID:90040744; PMID:2478717  
A;Accession: B32999  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <SA>  
A;Cross-references: UNIPROT:P20939; GB:X17664; NID:963974; PIDN:CAA35661.1; PID:g63975  
C;Superfamily: myelin basic protein  
Query Match 56.4%; Score 53; DB 2; Length 155;  
Best Local Similarity 53.3%; Pred. No. 0.13;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
Db 72 DSAVWHFFKQNIKVTPR 86

RESULT 11

G64440 hypothetical protein MJ1128 - Methanococcus jannaschii  
C;Species: Methanococcus jannaschii  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: G64440  
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Olson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Science 273, 1058-1073, 1996  
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
A;Reference number: A64300; MUID:96337999; PMID:8688087  
A;Accession: G64440  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Map position: REV1069975-169049  
A;Molecule type: DNA  
A;Residues: 1-308 <BUL>  
A;Cross-references: UNIPROT:Q58528; GB:U67555; GB:L77117; NID:g1591760; PIDN:AAB99130.1;  
C;Genetics:  
A;Map position: REV1069975-169049  
A;Start codon: GTG  
C;Superfamily: hypothetical protein MJ1128  
Query Match 47.9%; Score 45; DB 2; Length 308;  
Best Local Similarity 70.0%; Pred. No. 6.7;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 35 ENPVVHFFKQNIKVTPR 44

RESULT 12

A57246 beta-tectorin precursor - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: A57246  
R;Killick, R.; Legan, P.K.; Malenzak, C.; Richardson, G.P.  
J. Cell Biol. 129, 535-547, 1995  
A;Title: Molecular cloning of chick beta-tectorin, an extracellular matrix molecule of the

Qy 10 NIVTRRTP 17  
 Db 1 NIVTRRTP 8

**RESULT 15**  
 C89965  
 Query Match 46.8%; Score 44; DB 2; Length 329;  
 Best Local Similarity 53.8%; Pred. No. 11; Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 A;Cross-references: UNIPROT:P54097; GB:L38519; NID:g602439; PIDN:AAA92461;1; PID:g602440  
 C;Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage  
 C;Species: Neurospora crassa  
 C;Accession: T46577  
 R;Baker, D.L.; Paliotta, J.V.  
 Submitted to the EMBL Data Library, February 1997  
 A;Description: Molecular characterization of the arylsulfatase gene of *Neurospora crassa*  
 A;Reference number: Z23090  
 A;Accession: T46577  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-639 <BAK>  
 A;Cross-references: UNIPROT:O43113; EMBL:U83492; PIDN: AAC02716.1  
 A;Experimental source: strain wild type 74-OR23-1A  
 C;Genetics:  
 A;Gene: ars-1  
 A;Map position: 7  
 A;Intron: 115/1; 518/3  
 C;Function:  
 A;Description: EC 3.1.6.1 [validated, MUID:89384589]  
 A;Note: Genes are expressed under conditions of sulfur limitation and are under coordinate control  
 C;Keywords: sulfuric ester hydrolase

Query Match 46.8%; Score 44; DB 2; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 23; Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 A;Title: Identification of the sites in myelin basic protein that are phosphorylated by protein kinase C  
 A;Reference number: S12904  
 A;Accession: S12904  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <SAN>  
 A;Cross-references: UNIPROT:Q7M3M4  
 C;Keywords: phosphotransferase

Query Match 45.7%; Score 43; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.41; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 13**  
 T46577  
 A;Species: *Neurospora crassa*  
 C;Accession: T46577  
 R;Baker, D.L.; Paliotta, J.V.  
 Submitted to the EMBL Data Library, February 1997  
 A;Description: Molecular characterization of the arylsulfatase gene of *Neurospora crassa*  
 A;Reference number: Z23090  
 A;Accession: T46577  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-639 <BAK>  
 A;Cross-references: UNIPROT:O43113; EMBL:U83492; PIDN: AAC02716.1  
 A;Experimental source: strain wild type 74-OR23-1A  
 C;Genetics:  
 A;Gene: ars-1  
 A;Map position: 7  
 A;Intron: 115/1; 518/3  
 C;Function:  
 A;Description: EC 3.1.6.1 [validated, MUID:89384589]  
 A;Note: Genes are expressed under conditions of sulfur limitation and are under coordinate control  
 C;Keywords: sulfuric ester hydrolase

Query Match 45.7%; Score 43; DB 2; Length 85;  
 Best Local Similarity 35.7%; Pred. No. 3.3; Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 A;Title: Identification of the sites in myelin basic protein that are phosphorylated by protein kinase C  
 A;Reference number: S12904  
 A;Accession: S12904  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <SAN>  
 A;Cross-references: UNIPROT:Q7M3M4  
 C;Keywords: phosphotransferase

Query Match 45.7%; Score 43; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.41; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 14**  
 S12904  
 Protein kinase (EC 2.7.1.37) - starfish (*Pisaster ochraceus*)  
 C;Species: Pisaster ochraceus  
 C;Accession: S12904  
 R;Sanghadas, J.S.; Heberbold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
 FEBS Lett. 273, 223-226, 1990  
 A;Title: Identification of the sites in myelin basic protein that are phosphorylated by protein kinase C  
 A;Reference number: S12904  
 A;Accession: S12904  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <SAN>  
 A;Cross-references: UNIPROT:Q7M3M4  
 C;Keywords: phosphotransferase

Query Match 45.7%; Score 43; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.41; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



STRAIN-Sprague-Dawley; RX  
 MEDLINE:22941925; PubMed=14590679; DOI=10.1038/j.bbaexp.2003.08.010;  
 RA Matheus L., Blair G.E.;  
 RA "Identification and characterisation of a cDNA encoding a 17-kDa isoform of rat myelin basic protein.";  
 RT Blochim. Biophys. Acta 1630:47-53(2003).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley;  
 RA Matheus L.M., Blair G.E.;  
 RC Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 RL DR EMBL: AF039750; AA:8189-1; "Structural constituent of myelin sheath; IBA.  
 GO: GO:0019911; P:structural constituent of myelin sheath; IBA.  
 DR DR InterPro: IPRO00548; Myelin BP.  
 PFAM: PF01669; Myelin\_MBP; I.  
 PRINTS: PR00212; MYELINNMBP.  
 PRODOM: PD004542; Myelin\_BP; I.  
 PROSITE: PS00569; MYELIN\_MBP; I.  
 SEQUENCE: 158 AA; 17240 MW; 325658024ECCB1 CRC64;  
 SQ DSQ

Query Match 100 %; Score 94; DB 2; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKQIVTPRTP 17  
 DB 81 ENPVVHFFKQIVTPRTP 97

RESULT 3

QSP104 PRELIMINARY; PRT; 160 AA.

ID QSP104; PRELIMINARY; PRT; 160 AA.

QSP104; 06-F104; 05-JUL-2004 (TREMBREL. 27, Created)  
 DT 05-JUL-2004 (TREMBREL. 27, Last sequence update)

NCBI\_TaxID=95066;

[1] Sequence FROM N.A.  
 Buxarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
 Homo sapiens (Human).

OS Homo sapiens (Human).  
 OC Buxarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
 OC NCBI\_TaxID=95066;

RN SEQUENCE FROM N.A.  
 Hallbeck A., Ebert L., Mkandinya M., Schick M., Eisenstein S.,  
 Neubert P., Kettang K., Schatten R., Shen B., Henze S., Mar W.,  
 Korn B., Zuo D., Hu Y., DaBaer J.;  
 Submitted (JUN-2004) to the EMBL/GenBank/DDJB databases.

EMBL: CR53654; CAG38771.1; -  
 GO: GO:0019911; P:structural constituent of myelin sheath; IBA.  
 InterPro: IPRO00548; Myelin BP.  
 PFAM: PF01669; Myelin\_MBP; I.  
 PRINTS: PR00212; MYELINNMBP.  
 PRODOM: PD004542; Myelin\_BP; I.  
 PROSITE: PS00569; MYELIN\_MBP; I.  
 SEQUENCE: 160 AA; 17347 MW; 0107AAD6053CDB76 CRC64;

Query Match 100 %; Score 94; DB 2; Length 160;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKQIVTPRTP 17  
 DB 84 ENPVVHFFKQIVTPRTP 100

RESULT 4

MBP\_CAVPO STANDARD; PRT; 167 AA.

ID MBP\_CAVPO STANDARD; PRT; 167 AA.

P2518';  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

RA Myelin basic protein (MBP).  
 OS Cavia porcellus (Guinea Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.  
 OC NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE;  
 RX MEDLINE:84215086; PubMed=6202840;  
 RA Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;  
 RC "Sequence of guinea pig myelin basic protein.";  
 RL DR J. Neurochem. 43:100-105(1984).  
 RN [2]  
 RP SEQUENCE OF 7-156 FROM N.A.  
 RA DR STRAIN-Hatley-7156; TISSUE-spinal cord;  
 RA Kim G., Tanuma N., Matsumoto Y.;  
 RT "DNA vaccination using Guinea pig myelin basic protein coding region  
 in experimental autoimmune encephalomyelitis";  
 RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 RL RN [3]  
 RP SEQUENCE OF 45-87;  
 RA Shapira R., McKneally S.S., Chou F., Kibler R.F.;  
 RC RT "The contribution of phosphorylation and loss of COOH-terminal  
 arginine to the microheterogeneity of myelin basic protein.";  
 RT DR J. Biol. Chem. 250:7931-7938(1975).  
 CC CC -|- FUNCTION: IS, with the most abundant protein component of the  
 myelin membrane in the CNS. Has a role in both the formation and  
 stabilization of this compact multilayer arrangement of bilayers.  
 CC CC Each splice variant or charge isomer may have a specialized  
 function in the assembly of an optimized, biochemically functional  
 myelin membrane (By similarity).  
 CC CC -- SUBUNIT: Homodimer (By similarity).  
 CC CC -- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 CC CC -- TISSUE SPECIFICITY: Found in both the central and the peripheral  
 nervous system.  
 CC CC -- PTM: At least 5 charge isomers; C1 (the most cationic, least  
 modified, and most abundant form), C2, C3, C4 and C5 (the least  
 cationic form); are produced as a result of optional  
 posttranslational modifications such as phosphorylation of serine  
 or threonine residues, deamidation of glutamine or asparagine  
 residues, citrullination and methylation of arginine residues. C1  
 and C2 are unphosphorylated, C3 and C4 are monophosphorylated and  
 C5 is phosphorylated at two positions.  
 CC CC -- SIMILARITY: Belongs to the myelin basic protein family.  
 CC CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).)  
 CC DR EMBL: AF074337; AAC26130.1; -  
 DR PIR: A37246; A37246.  
 DR HSPB; P02686; 10CL.  
 DR InterPro: IPRO00548; Myelin\_BP.  
 DR PFAM: PF01669; Myelin\_MBP; I.  
 DR PRINTS: PR00212; MYELINNMBP.  
 DR PRODOM: PD004542; Myelin\_BP; I.  
 DR PROSITE: PS00569; MYELIN\_MBP; I.  
 DR Acetylation; Autoimmune encephalomyelitis; Citrullination;  
 KW Direct Protein sequencing; Methylation; Myelin; Phosphorylation;  
 KW Structural protein.  
 FT DOMAIN 45 87 induces experimental autoimmune  
 FT encephalomyelitis (EAE) 1.

FT	DOMAIN	114	122	Induces experimental autoimmune encephalomyelitis (EAE) 2.	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	1	1	N-acetylated alanine.	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	7	7	Phosphoserine (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	25	25	Citrulline (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	31	31	Citrulline (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	56	56	Phosphoserine (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	97	97	Phosphothreonine (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	102	102	Deamidated glutamine (partial) (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	106	106	Symmetric dimethylarginine (By similarity).	CC	-!- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.
FT	MOD_RES	114	114	Phosphoserine (By similarity).	DR	-!- PTM: The N-Terminal is blocked.
FT	MOD_RES	129	129	Citrulline (By similarity).	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
FT	MOD_RES	144	144	Deamidated glutamine (partial) (By similarity).	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
FT	MOD_RES	155	156	Citrulline (By similarity).	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
FT	MOD_RES	158	158	Phosphoserine (By similarity).	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
FT	MOD_RES	162	162	Phosphoserine (By similarity).	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
FT	MOD_RES	167	167	Citrulline (By similarity).	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
SQ	SEQUENCE	167 AA;	18213 MW;	EC3C97ACD2C08EA6 CRC64;	DR	-!- SIMILARITY: Belongs to the myelin basic protein family.
Query	Match	100 0%;	Score 94; DB 1; Length 167;		PRINTS; PR00212; MYELINMBP.	
Best	Local Similarity	100 0%;	Pred. No. 1.3e-07;		PRODOM; P00452; Myelin BP; 1.	
Matches	17;	Conservative	0;	Mismatches 0;	PS00679; MYELIN MBP; 1.	
Qy	1	ENPVWIRPKNIKVTPRIP 17		INDELS 0;	KW	Acetylation: Autoimmune encephalomyelitis; Citrullination; Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.
Db	82	ENPVWIRPKNIKVTPRIP 98		GAPS 0;	DOMAIN	45 86
RESULT	5				DR	PRINTS; PR00212; MYELINMBP.
ID	MBP_RABIT		STANDARD;	PRT;	DR	PRODOM; P00452; Myelin BP; 1.
AC	P25274;				DR	PS00679; MYELIN MBP; 1.
DT	01-MAY-1992	(Rel. 22, Created)			DR	HSSP; P01686; IQLC; Myelin BP.
DT	16-OCT-2001	(Rel. 40, Last sequence update)			DR	InterPro; IPR00548; Myelin BP.
DT	05-JUL-2004	(Rel. 44, Last annotation update)			DR	Protein Data Bank; P01669; Myelin MBP; 1.
DE	Myelin basic protein (MBP) (Myelin A1 protein).				DR	Protein Data Bank; P01669; Myelin MBP; 1.
GN	Name=MBP;				DR	Protein Data Bank; P01669; Myelin MBP; 1.
OS	Oryctolagus cuniculus (Rabbit)				DR	Protein Data Bank; P01669; Myelin MBP; 1.
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.				DR	Protein Data Bank; P01669; Myelin MBP; 1.
OX	NCBI_TAXID=986;				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RN	[1]				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RP	PRELIMINARY SEQUENCE.				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RC	TISSUE=Sciatic nerve;				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RX	MEDLINE=73190057; PubMed=4662101;				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RT	"The proposed amino acid sequence of the P1 protein of rabbit sciatic nerve myelin.";				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RL	Arch. Biochem. Biophys. 153:590-598(1972).				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RN	[2]				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RP	SEQUENCE OF 45-86.				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RA	Shapira R., McKNALLY S.S., Chou F., KIBLER R.F.:				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RT	"Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RT	Sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RL	J. Biol. Chem. 246:4630-4640(1971).				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RN	[3]				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RP	PHOSPHORYLATION.				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RX	MBLNE=83108902; PubMed=618581;				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RA	Marston R.E., Law M.J., Deibler G.E.:				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RT	"Identification of multiple in vivo phosphorylation sites in rabbit myelin basic protein.";				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RT	myelin basic protein function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).				DR	Protein Data Bank; P01669; Myelin MBP; 1.
RX	NCBI_TAXID=9913;				DR	Protein Data Bank; P01669; Myelin MBP; 1.
CC	-1- FUNCTION: is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.				DR	Protein Data Bank; P01669; Myelin MBP; 1.
CC	Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).				DR	Protein Data Bank; P01669; Myelin MBP; 1.
CC	-1- SUBUNIT: Homodimer (By similarity).				DR	Protein Data Bank; P01669; Myelin MBP; 1.
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.				DR	Protein Data Bank; P01669; Myelin MBP; 1.

- RP REVISION.  
 RX MEDLINE=4070588; PubMed=4129204;  
 RA Brostoff S.W.; Reuter W.; Hichens M.; Eylar E.H.;  
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";  
 RL J. Biol. Chem. 249:5559-5567(1974).  
 RN [31] SEQUENCE OF 4-56 FROM N.A.  
 RA Pietrowski D.; Medigorce I.; Poerster M.;  
 RT "A new MBP allele in *Bos taurus* is characterized by BoNT PCR-RFLP.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [41] SEQUENCE OF 43-87.  
 RA Shapira R.; McNeally S.S.; Chou F.C.-H.; Kibler R.F.;  
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid  
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
 RL J. Biol. Chem. 246:4630-4640(1971).  
 RN [15] SEQUENCE OF 38-58 AND 119-141.  
 RP TISSUE=Brain;  
 RX MEDLINE=93003019; PubMed=1382581;  
 RA Pirollet P.; Derancourt J.; Haiech J.; Job D.; Margolis R.L.;  
 RT "Calmodulin regulated effectors of microtubule stability in  
 bovine brain.";  
 RL Biochemistry 31:8849-8855(1992).  
 RN [6] SEQUENCE OF 30-42; 74-89 AND 114-129.  
 RX MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;  
 RA Preiss K.; Barouch W.; Martin B.M.; Greene L.E.; Eisenberg E.;  
 RT "Purification of a new clathrin assembly protein from bovine brain  
 coated vesicles and its identification as myelin basic protein.";  
 RL J. Biol. Chem. 270:30551-30556(1995).  
 RN [7] SEQUENCE OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.  
 RX MEDLINE=70178977; PubMed=542707;  
 RA Eyer E.H.; Cocciam J.; Jackson J.J.; Westall F.C.; Robinson A.B.;  
 RT "Experimental allergic encephalomyelitis: synthesis of disease-  
 inducing site of the basic protein.";  
 RL Science 168:1220-1223(1970).  
 RN [8] METHYLATION.  
 RX MEDLINE=71153946; PubMed=4994464;  
 RA Brostoff S.W.; Eyer E.H.;  
 RT "Localization of methylated arginine in the A1 protein from myelin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).  
 RN [9] POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=6167591; PubMed=57115;  
 RA Chou F.-C.-H.; Chou C.-H.J.; Shapira R.; Kibler R.F.;  
 RT "Biosynthesis of myelin basic protein.";  
 RL J. Biol. Chem. 251:2671-2679(1976).  
 RN [10] SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97.  
 RX MEDLINE=91060584; PubMed=1700797;  
 RA Erickson A.K.; Payne D.M.; Martino P.A.; Rossomando A.J.;  
 RA Shabanian J.; Weber M.J.; Hunt D.F.; Sturgill T.W.;  
 RT "Identification by mass spectrometry of threonine 97 in bovine myelin  
 basic protein as a specific phosphorylation site for mitogen-activated  
 protein kinase.";  
 RL J. Biol. Chem. 265:19728-19735(1990).  
 RN [11] POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=81153125; PubMed=9483392; DOI=10.1021/bi972347t;  
 RA Zand R.; Li M.X.; Jin X.; Lubman D.;  
 RT "Determination of the sites of posttranslational modifications in the  
 RT charge isomers of bovine myelin basic protein by capillary  
 RT electrophoresis-mass spectroscopy.";  
 RL Biochemistry 37:2441-2449(1998).  
 RN [11] DIMERIZATION.  
 RX MEDLINE=80198320; PubMed=6155143;  
 RA Smith R.;  
 RT "Sedimentation analysis of the self-association of bovine myelin basic  
 protein.";

RL Biochemistry 19:1866-1881(1980).  
 RX FUNCTION: Is, with PLP, the most abundant protein component of the  
 CC myelin membrane in the CNS. Has a role in both the formation and  
 CC stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized functional  
 CC function in the assembly of an optimized, biochemically functional  
 CC myelin membrane (BY similarity).  
 CC SUBUNIT: Homodimer; self-associates in the presence of lysolipid.  
 CC SUBCELLULAR LOCATION: Cyttoplasmic side of myelin.  
 CC TISSUE SPECIFICITY: Found in both the central and the peripheral  
 nervous system.  
 CC PTM: At least 6 charge isomers; C1 (the most cationic and least  
 modified form), C2, C3, C4, C5 and C6 (the least cationic form);  
 CC are produced as a result of optional posttranslational  
 CC modifications, such as phosphorylation of serine or threonine  
 residues, deamidation of glutamine or asparagine residues,  
 CC citrullination and methylation of arginine residues.  
 CC -1- SIMILARITY: Belongs to the myelin basic protein family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR PROTEIN: P02686; LOC1  
 DR HSSP: P02686; ICL1  
 DR InterPro: IPR000543; Myelin BP.  
 DR PFAM: PF01669; Myelin MBP; 1.  
 DR PRINS: PR00212; MYELIN MBP; 1.  
 DR PROSITE: PS00569; MYELIN MBP; 1.  
 KW Acetylation: Autoimmune encephalomyelitis; Citrullination;  
 KW Direct protein sequencing; Methylation; Myelin; Phosphorylation;  
 KW Encephalomyelitis (BAE) 1.  
 KW Structural protein.  
 PT DOMAIN 43 87  
 PT DOMAIN 114 122  
 PT DOMAIN 114 122  
 PT MOD\_RES 1 1  
 PT MOD\_RES 7 7  
 PT MOD\_RES 23 23  
 PT MOD\_RES 29 29  
 PT MOD\_RES 54 54  
 PT MOD\_RES 97 97  
 PT MOD\_RES 102 102  
 PT MOD\_RES 106 106  
 PT MOD\_RES 106 106  
 PT MOD\_RES 114 114  
 PT MOD\_RES 129 129  
 PT MOD\_RES 146 146  
 PT MOD\_RES 158 158  
 PT MOD\_RES 160 160  
 PT MOD\_RES 164 164  
 PT MOD\_RES 169 169  
 PT SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;  
 Query Match 100.0%; Score 94; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 1-4e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ENPVVHFFKQIVTPRTP 17  
 Db 82 ENPVVHFFKQIVTPRTP 98

RESULT 7  
 ID MBP\_PANTR STANDARD; PRT; 171 AA.

AC	P06905;	DT	01-JAN-1988 (Rel. 06, Created)
DT	05-MAY-2000 (Rel. 39, Last sequence update)	DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)	DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Myelin basic protein (MBP).	DE	Myelin basic protein (MBP).
GN	Name=MBP;	GN	Name=MBP;
OS	Pan troglodytes (Chimpanzee); Bukarota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	OS	Bukarota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC	NCBI_TaxID:9598;	OC	NCBI_TaxID:9823;
RN	[1]	RN	[1]
RP	PRELIMINARY_SEQUENCE.	RP	SEQUENCE, AND METHYLATION OF ARG-107.
RX	MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8;	RX	TISSUE-Brain;
RA	"Westall F.C., Thompson M.", Kalter S.S.;	RA	MEDLINE=85056964; PubMed=2578056;
RT	"The proposed sequence of the encephalitogenic protein from chimpanzee brain".	RT	Kira J.-I., Krutzsch H.C., Martenson R.E.;
RL	Life Sci. 17:219-223(1975).	RL	"Amino acid sequence of porcine myelin basic protein.";
RN	-!- FUNCTION: Is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.	RN	J. Neurochem. 44:134-142(1985).
RP	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	RP	ERRATUM.
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.	CC	RA Kira J.-I., Deibler G.B., Krutzsch H.C., Martenson R.E.;
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	RL J. Neurochem. 44:1663-1663 (1985).
CC	-!- SUBUNIT: Homodimer (By similarity).	CC	-!- FUNCTION: Is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.
CC	-!- SIMILARITY: Belongs to the myelin basic protein family.	CC	-!- PTM: As in other animals, several charge isomers may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	-!- SUBUNIT: Homodimer (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	-!- SIMILARITY: Belongs to the myelin basic protein family.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR HSSP; P02686; IQLC.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR InterPro; IPK00548; Myelin BP.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR PRATIS; PR00212; MYELINMBP.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR PROSIT; A01640; MBPBP.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR HSSP; P02686; IQLC.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR PROSIT; A01640; MYELINMBP; 1.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR PROSIT; P0004542; MYELIN BP; 1.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	DR Acetylation; Citrullination; Direct Protein sequencing; Methylation; KW Myelin; Phosphorylation; Structural protein.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 1 1 N-acetylalanine.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 7 7 Phosphoserine (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 25 25 Citrulline (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 31 31 Diamidated glutamine (partial) (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 55 55 Omega-N-methylated arginine.
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 98 98 Phosphoserine (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 103 103 Diamidated glutamine (partial) (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 107 107 Omega-N-methylarginine (partial).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 107 107 Symmetric dimethylarginine (partial).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 115 115 Phosphoserine (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 130 130 Phosphothreonine (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 148 148 Diamidated glutamine (partial) (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 160 160 Citrulline (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 162 162 Phosphoserine (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 166 166 Phosphoserine (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT MOD_RES 171 171 Citrulline (By similarity).
CC	-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.	CC	FT SEQUENCE 171 AA; 18487 MW; 287AEDB2F24028D9 CRC64;
QY	Query Match Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	Query Match Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 ENPVVHFFKNIVPRTP 17	Db	1 ENPVVHFFKNIVPRTP 17
Db	83 ENPVVHFFKNIVPRTP 99	Db	83 ENPVVHFFKNIVPRTP 99
RESULT 8		QY	
MAP_PIG	STANDARD;	PRT;	171 AA.
ID	MAP_PIG		

RESULT 9

Q62R3 PRELIMINARY; PRT; 173 AA.

ID Q62R3; PRELIMINARY; PRT; 173 AA.

AC Q62R3; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

DT 05-JUL-2004 (TREMBrel; 27, Created)

DT 05-JUL-2004 (TREMBrel; 27, Last sequence update)

DE Myelin basic protein.

OS Sus scrofa (Pig)

OC Buiaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.

OX NCBI\_TaxID=983;

[1]

SEQUENCE FROM N.A.

RP Kim J.G., Nonneman D., Vallet J.L., Rohrer G.A., Christenson R.K.;

RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY03684; AAY28338; 1; -.

GO; GO:0019911; F:structural constituent of myelin sheath; IEA.

DR InterPro; IPR00548; Myelin BP.

PEM; PR01669; Myelin MBP; 1.

DR PRINTS; PRO0012; MYELINMBP.

PRODOM; PD00542; Myelin\_BP; 1.

DR PROSITE; PS00569; MYELIN\_MBP; 1.

DR NON\_TER; 1

SQ SEQUENCE 173 AA; 18731 MW; 66B4D016B660B1AA CRC64;

Query Match Best Local Similarity 100.0%; Score 94; DB 2; Length 173; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKQIVTPRTP 17

Db 85 ENPVVHFFKQIVTPRTP 101

RESULT 10

Q6PK23 PRELIMINARY; PRT; 180 AA.

ID Q6PK23; PRELIMINARY; PRT; 180 AA.

AC Q6PK23; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

DT 05-JUL-2004 (TREMBrel; 27, last sequence update)

DT 05-JUL-2004 (TREMBrel; 27, Last annotation update)

DE MBP protein (Fragment).

GN Name=MBP;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A.

RP TISSUE=SKIN; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX STRAUBERG L.R., Feingold E.A., Grouse L.H., Derge J.G., Klaubner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tsoiuky L., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley C., Hale S., Garcia A.M., Gay J.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.J., Staltska U., Smalius D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). RP SEQUENCE FROM N.A.

RESULT 11

MBP\_RAT STANDARD; PRT; 194 AA.

ID MBP\_RAT; STANDARD; PRT; 194 AA.

AC P02688; O9Z1J4; O9Z1J5; O9Z1J6; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

DT 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, last sequence update)

DT 05-JUL-2004 (Rel. 44, last annotation update)

DE Myelin basic protein S (MBP S).

GN Name=MBP;

OS Rattus norvegicus (Rat)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

[1]

SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4).

RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4).

RA Lobell A.M., Wigzell H.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

RL [2]

RN SEQUENCE FROM N.A. (ISOFORM 4).

RP SEQUENCE FROM N.A. (ISOFORM 4).

RX MEDLINE=702649; PubMed=2429678;

RA Schach M., Budzinski R.M., Stooffel W., Cloned proteolipid protein and myelin basic protein cDNA.

RA RT Transcription of the two genes during myelination.;

RL RT Biol. Chem. Hoppe-Seyler 367:825-834(1986).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 4).

RX MEDLINE=4402684; PubMed=619889; DOI=10.1016/0092-8674(83)90536-5;

RA Roach A., Boylan K.B., Horvath S., Prusiner S.B., Hood L.E.; "Characterization of cloned cDNA representing rat myelin basic protein: absence of expression in brain of shiverer mutant mice.";

RT Cell 34:799-806(1983).

RL RN [4]

RP SEQUENCE (ISOFORM 4).

RX MEDLINE=512759; PubMed=4141893;

RA Dunkley P.R., Carnegie P.R.; "Amino acid sequence of the smaller basic protein from rat brain myelin.;" Biochem. J. 141:243-255(1974).

RL RN [5]

RP SEQUENCE OF 130-194 FROM N.A.

RC STRAIN=Lewis; TISSUE=Brain; MEDLINE=66078224; PubMed=7570863;

RA Malorka J., Dornmair K.; "Alternative splicing and cDNA sequence of myelin basic protein gene of the Lewis rat." RL Autoimmunity 20:67-68(1995).

RN [6]

RP SEQUENCE OF 45-111 (ISOFORM 4).

RX MEDLINE=3180720; PubMed=4123324;

RA McFailin D.E., Blank S.E., Kubler R.F., McKneally S.S., Shapira R.; "Experimental allergic encephalomyelitis in the rat: response to



RESULT 2  
US-10-000-439-13  
; Sequence 13, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067\_00A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 13  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-000-439-13

Query Match 100.0%; Score 94; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIKTPRTP 17  
Db 1 ENPVVHFFKNIKTPRTP 17

RESULT 3  
US-10-362-264-1  
; Sequence 1, Application US/10362264  
; Publication No. US20030191063A1  
; GENERAL INFORMATION:  
; APPLICANT: Wraith, David  
; APPLICANT: Anderson, Stephen  
; APPLICANT: Mazza, Graziella  
; APPLICANT: Ponford, Mary  
; APPLICANT: Streeter, Heather  
; APPLICANT: The University of Bristol  
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD  
; FILE REFERENCE: 1433-004US1  
; CURRENT APPLICATION NUMBER: US/10/362,264  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03702  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 0020618-5  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 0114547-3  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-362-264-1

Query Match 100.0%; Score 94; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIKTPRTP 17  
Db 1 ENPVVHFFKNIKTPRTP 17

RESULT 4  
US-10-233-892A-2  
; Sequence 2, Application US/10233892A  
; Publication No. US2004043431A1  
; GENERAL INFORMATION:

RESULT 5  
US-10-482-044-5  
; Sequence 5, Application US/10482044  
; Publication No. US20040235713A1  
; GENERAL INFORMATION:  
; APPLICANT: Anna Maria PAPINI et al  
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or  
; therapeutic treatment of multiple sclerosis  
; FILE REFERENCE: 2784 PTWO  
; CURRENT APPLICATION NUMBER: US/10/482,044  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: PCT/EP 02/06767  
; PRIOR FILING DATE: 2002-05-19  
; PRIOR APPLICATION NUMBER: FI2001A000114  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 5  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: glycopeptide  
; FEATURE:  
; NAME/KEY: CARBOHYD  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl

US-10-482-044-5

Query Match 100.0%; Score 94; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIKTPRTP 17  
Db 1 ENPVVHFFKNIKTPRTP 17

RESULT 6  
US-09-740-003-2  
; Sequence 2, Application US/09740003  
; Publication No. US2002003982A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, SYAMAL  
; APPLICANT: RASTETTER, WILLIAM H.  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; FILE REFERENCE: 37003/275802

CURRENT APPLICATION NUMBER: US/09/740,003  
 CURRENT FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: 09/024,220  
 PRIOR FILING DATE: 1998-02-17  
 PRIOR APPLICATION NUMBER: 08/476,674  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR FILING DATE: 1994-12-07  
 PRIOR APPLICATION NUMBER: 08/919,787  
 PRIOR FILING DATE: 1997-08-29  
 PRIOR APPLICATION NUMBER: 07/735,069  
 PRIOR FILING DATE: 1991-07-25  
 NUMBER OF SEQ ID NOS: 2  
 SEQ ID NO 2  
 SOFTWARE: PatentIn Ver. 2.1  
 LENGTH: 19  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: peptide  
 US-09-740-003-2

Query Match 100.0%; Score 94; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 US-09-768-872-1  
 ; Sequence 1, Application US/09768872  
 ; Patent No. US20020055462A1  
 GENERAL INFORMATION:  
 APPLICANT: Aharoni, Rina  
 APPLICANT: Teitelbaum, Dvora  
 APPLICANT: Arnon, Ruth  
 APPLICANT: Sela, Michael  
 APPLICANT: Fridkin-Harelli, Masha  
 APPLICANT: Strominger, Jack  
 TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1  
 TITLE OF INVENTION: and Related Copolymers and Peptides  
 FILE REFERENCE: 162/493/762  
 CURRENT APPLICATION NUMBER: US/09/768,872  
 CURRENT FILING DATE: 2001-01-23  
 PRIOR APPLICATION NUMBER: US 60/093,859  
 PRIOR FILING DATE: 1998-07-23  
 PRIOR APPLICATION NUMBER: US 60/101,825  
 PRIOR FILING DATE: 1998-09-25  
 PRIOR APPLICATION NUMBER: US 60/102,960  
 PRIOR FILING DATE: 1998-10-02  
 PRIOR APPLICATION NUMBER: US 60/106,350  
 PRIOR FILING DATE: 1998-10-30  
 PRIOR APPLICATION NUMBER: US 60/108,184  
 PRIOR FILING DATE: 1998-11-12  
 PRIOR APPLICATION NUMBER: US 60/123,675  
 PRIOR FILING DATE: 1999-03-09  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: WordPerfect 8.0 for Windows  
 SEQ ID NO 1  
 LENGTH: 19  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: synthetic peptide (MBP residues 84-102)  
 US-09-768-872-1

Query Match 100.0%; Score 94; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 US-09-766-378A-32  
 ; Sequence 32, Application US/09766378A  
 ; Patent No. US20020091079A1  
 GENERAL INFORMATION:  
 APPLICANT: Rhode, Peter R.  
 APPLICANT: Acevedo, Jorge  
 APPLICANT: Burkhardt, Martin  
 APPLICANT: Jiao, Jin-an  
 APPLICANT: Wong, Hing C.  
 TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Dike, Bronstein, Roberts & Cushman, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: usa  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/960,190  
 FILING DATE: 19-Jan-2001  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Corless, Peter F.  
 REGISTRATION NUMBER: 33,860  
 REFERENCE/DOCKET NUMBER: 48002-DIV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
 US-09-766-378A-32

Query Match 100.0%; Score 94; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 US-10-239-313A-143  
 ; Sequence 13, Application US/10239313A  
 ; Publication No. US20030175285A1  
 GENERAL INFORMATION:  
 APPLICANT: KLINGNER - HAMOUR, Christine  
 APPLICANT: CORVATA, Nathalie  
 APPLICANT: BECK, Alain

US-03-766-378A-2B  
; Sequence 28, Application US/09766378A  
; Patent No. US2000091079A1  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; Aceredo, Jorge  
; Burhardt, Martin  
; Jiao, Jin-an  
; Wong, Hing C.  
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND  
; METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 110 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: RatSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,378A  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/960,190  
; FILING DATE: 29-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coless, Peter F.  
; REGISTRATION NUMBER: 33,860  
; REFERENCE DOCKET NUMBER: 48002-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
; US-09-766-378A-28  
; Query Match 100.0%; Score 94; DB 16; Length 19;  
; Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; QY 1 ENPVVHFFKQIVTPRTP 17  
; DB 2 ENPVVHFFKQIVTPRTP 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
; US-10-743-398-2  
; Query Match 100.0%; Score 94; DB 16; Length 19;  
; Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; QY 1 ENPVVHFFKQIVTPRTP 17  
; DB 2 ENPVVHFFKQIVTPRTP 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 30  
; LENGTH: 20  
; RESULT 10

US-10-743-398-2  
; Sequence 2, Application US/10743398  
; Publication No. US2004019731A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, SYAMAL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: BLACK, AMELIA  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; FILE REFERENCE: 370037430  
; CURRENT APPLICATION NUMBER: US/10/743,398  
; CURRENT FILING DATE: 2003-12-23  
; PRIORITY APPLICATION NUMBER: 09/740,003  
; PRIORITY FILING DATE: 2000-12-20  
; PRIORITY APPLICATION NUMBER: 09/024,220  
; PRIORITY FILING DATE: 1998-02-17  
; PRIORITY APPLICATION NUMBER: 08/476,674  
; PRIORITY FILING DATE: 1995-06-07  
; PRIORITY APPLICATION NUMBER: 08/351,001  
; PRIORITY FILING DATE: 1994-12-07  
; PRIORITY APPLICATION NUMBER: 08/919,787  
; PRIORITY FILING DATE: 1997-08-29  
; PRIORITY APPLICATION NUMBER: 07/735,069  
; PRIORITY FILING DATE: 1991-07-25  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
; US-10-743-398-2  
; Query Match 100.0%; Score 94; DB 16; Length 19;  
; Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; QY 1 ENPVVHFFKQIVTPRTP 17  
; DB 2 ENPVVHFFKQIVTPRTP 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 30  
; LENGTH: 19  
; RESULT 11

US-09-836-433-30  
; Sequence 30, Application US/09836433  
; Publication No. US20030049797A1  
; GENERAL INFORMATION:  
; APPLICANT: Yuki, Yoshikazu  
; APPLICANT: Ueda, Shigezo  
; TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE  
; FILE REFERENCE: NO. US20030049797A1 Assigned  
; CURRENT APPLICATION NUMBER: US09/836,433  
; CURRENT FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 30  
; LENGTH: 20  
; RESULT 12

QY	1	ENPVVHFFKRNIVPRTP 17	100.0%; Score 94; DB 7; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e-05; Mismatches 0; Indels 0; Gaps 0;
Db	1	ENPVVHFFKRNIVPRTP 17	Best Local Similarity 100.0%; Pred. No. 6.1e-05; Mismatches 0; Indels 0; Gaps 0;
RESULT 9			
ID	ADK67704	standard; peptide; 17 AA.	
XX			
AC	ADK67704;		
DT	06-MAY-2004	(first entry)	
XX			
DE	Human myelin basic protein peptide fragment MBP-1 (aa110-126).		
XX			
KW	Human; myelin basic protein; vaccine; multiple sclerosis; T cell.		
OS	Homo sapiens.		
XX			
PN	WO200415070-A2.		
XX			
PD	19-FEB-2004.		
PP	06-AUG-2003; 2003WO-US024548.		
XX			
PR	08-AUG-2002; 2002US-0402521P.		
XX			
PA	(BAYU ) BAYLOR COLLEGE MEDICINE.		
PA	(OPEX-) OPEXA PHARM INC.		
XX			
PI	Zhang JZ;		
XX			
DR	WPI; 2004-180654/17.		
XX			
PT	Isolating one or more T cells specific for an antigen of interest comprising incubating a T cell sample with an antigen, useful for diagnosing or treating multiple sclerosis, psoriasis, thyroiditis, diabetes and rheumatoid arthritis.		
PT	Isolating one or more T cells specific for an antigen of interest comprising incubating a T cell sample with an antigen, useful for diagnosing or treating multiple sclerosis, psoriasis, thyroiditis, diabetes and rheumatoid arthritis.		
PS	Example 1; SEQ ID NO 1; 38pp; English.		
XX			
CC	The present invention is direct to methods of isolating antigen specific T cells, especially T cells specific for self or autoantigens. This comprises incubating a sample of T cells obtained from a patient with the antigen and selecting T cells that express one or more of first markers selected from CD69, CD4, CD25, CD36 and HLA-DR, and one or more second markers selected from interleukin-2, interferon-gamma, tumour necrosis factor alpha, interleukin-5, interleukin-10 and interleukin-12. The methods are useful for isolating autoreactive T cells which play a role in the pathogenesis of autoimmune diseases. The methods also permit the diagnosis of autoimmune disease as well as monitoring the progression of the disease and for monitoring the efficacy of treatment. The methods allow the preparation of autologous T cell vaccines for the treatment of T cell related autoimmune diseases. Vaccine preparation involves the isolation of antigen-specific T cells optionally followed by culturing steps which allow the expansion of the population of isolated antigen-specific T cells. An example from the invention describes the isolation of myelin-reactive T cells for T cell vaccination. Peripheral blood mononuclear cells were isolated from the blood of multiple sclerosis patients and incubated with peptides comprising known immunodominant regions of 3 myelin proteins. These included the present peptide, which comprises amino acids 110-126 of human myelin basic protein. Cells were then selected for the expression of gene products indicative of activated T cells, and myelin-reactive T cells were propagated in culture. The methods and compositions of the invention are useful for the diagnosis and/or treatment of autoimmune diseases or T cell associated conditions such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus erythematosus, autoimmune thyroiditis, Grave's disease, inflammatory bowel disease, diabetes and rheumatoid arthritis.		
CC	Sequence 17 AA;		
CC	Query Match	100.0%; Score 94; DB 8; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e-05; Mismatches 0; Indels 0; Gaps 0;	
SQ	ENPVVHFFKRNIVPRTP 17	Best Local Similarity 100.0%; Pred. No. 6.1e-05; Mismatches 0; Indels 0; Gaps 0;	
RESULT 10			
ID	ADL18291		
XX			
AC	ADL18291;		
XX			
DE	Human myelin basic protein (MBP), peptide #2.		
XX			
KW	Demyelinating disease; neuron-specific antigen; human; myelin basic protein; MBP; myelin oligodendrocyte glycoprotein; myelin associated glycoprotein; MAG; proteolipid protein; PLP; small heat shock protein; transaldolase; glial fibrillary protein; S-100 protein; cross-reactive peptide; glutamate receptor; phosphodiesterase; multiple sclerosis.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004043431-A1.		
XX			
PD	04-MAR-2004.		
XX			
PF	29-AUG-2002; 2002US-00233892.		
XX			
PR	29-AUG-2002; 2002US-00233892.		
XX			
PA	(YVD/ ) VOJDANI A.		
XX			
PS	Claim 6; SEQ ID NO 2; 27pp; English.		
PI	Vojdani A;		
XX			
DR	WPI; 2004-313756/29.		
XX			
PT	Diagnosing likelihood and severity of demyelinating disease, by determining antibodies against neuron-specific antigen, comparing level of detected antibodies with normal level for detecting absence/likelihood of demyelinating disease.		
PT	Diagnosing likelihood and severity of demyelinating disease, by determining antibodies against neuron-specific antigen, comparing level of antibodies with the normal level of antibodies, where normal level of antibodies for neuron-specific antigen indicate optimal conditions, lower than or higher than normal level of antibodies for the antigen indicate an absence of or a likelihood of demyelinating diseases, respectively.		
CC	The present invention relates to a method of diagnosing the likelihood and severity of demyelinating diseases. The method involves determining antibodies against neuron-specific antigen in sample, comparing the level of antibodies with the normal level of antibodies, where normal level of antibodies for neuron-specific antigen indicate optimal conditions, lower than or higher than normal level of antibodies for the antigen indicate an absence of or a likelihood of demyelinating diseases, respectively.		
CC	The neuron-specific antigen is chosen from myelin basic protein (MBP), myelin oligodendrocyte glycoprotein, myelin associated glycoprotein (MAG), proteolipid protein (PLP), small heat shock protein, transaldolase, glial fibrillary protein, S-100 protein, cross-reactive peptide from dietary protein, cross-reactive peptide from infectious agent, glutamate receptor, and phosphodiesterase. The immunoassay is an enzyme linked immunosorbent assay (ELISA) test. The method is useful for diagnosing the likelihood and severity of demyelinating diseases such as multiple sclerosis in a patient. The present sequence represents a peptide from human MBP.		
SQ	Sequence 17 AA;		

		Query Match	100.0%; Score 94; DB 8; Length 17;	DE
		Best Local Similarity	100.0%; Pred. No. 6.1e-09; Mismatches 0; Indels 0; Gaps 0;	XX
		Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KW
		1 ENPVVHFFKKNIVPRTP 17	CD4+ T-cell; autoimmune disease; demyelination; central nervous system; CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG; relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PUP; diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome; psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG; myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.	KW
		2 ENPVVHFFKKNIVPRTP 17	diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome; psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG; myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.	KW
RESULT 11				OS
AAR44115	ID	AAR44115 standard; peptide; 18 AA.		XX
	AC	AAR44115;		PN
	KK			XX
	XX	25-MAR-2003 (revised)		XX
	DT	09-MAY-1994 (first entry)		PP
	DE	Human myelin basic protein residues 85-102.		XX
	KW	hMBP; suppression; auto immune response; multiple sclerosis; immunodominant epitope; T-cell proliferation; CD4; T-cells.		PR
	KX	Homo sapiens.		PR
	PS	W09321222-A1.		PR
	PN	28-OCT-1993.		PR
	XX	09-APR-1993; 93WO-US003369.		PT
	XX	09-APR-1992; 92US-00865318.		PT
	XX	(AUTO-) AUTOIMMUNE INC.		PT
	PA	Weiner HL, Hafler DA, Miller A, Al-Sabbagh A;		PI
	CC	OR		PI
	CC	WPI; 1993-351657/44.		XX
	CC	New peptide(s) derived from human myelin basic protein - used for suppressing auto-immune response, partic. in treating multiple sclerosis.		DR
	CC	Claim 1; Page 29; 118pp; English.		XX
	CC	The peptide represents residues 85-102 of human myelin basic protein (hMBP). The fragment comprises an immunodominant epitope of hMBP which was identified by overlapping 20-mer oligopeptide sequence analysis using T-cell line assays. The peptide can be used to stop proliferation of human T-cells specific for MBP or to elicit active suppression of such T-cells. They are also used partic. for the treatment of multiple sclerosis. The peptide is also useful for identifying CD4+ T-cells reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to correct PN field.)		XX
	SQ	Sequence 18 AA;		XX
	QQ	Query Match 100.0%; Score 94; DB 2; Length 18; Best Local Similarity 100.0%; Pred. No. 6.5e-09; Mismatches 0; Indels 0; Gaps 0;		XX
	DB	1 ENPVVHFFKKNIVPRTP 17	Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG; relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PUP; diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome; psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG; myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.	KW
RESULT 12				SYNTHETIC.
AAR95357	ID	AAR95357 standard; peptide; 18 AA.		W09321273-A2.
	AC	AAR95357;		
	XX	16-DEC-1996 (first entry)		
RESULT 13				Residues 83-100 of myelin basic protein.
AAW73600	ID	AAW73600 standard; peptide; 18 AA.		DE
	XX	AAW73600;		XX
	AC			XX
	XX	18-MAR-1999 (first entry)		DT
	XX	Human myelin basic protein fragment.		DE

XX Myelin basic protein; MBP; human; immunodominant region; inhibitor;  
 KW immunosuppressant agent; multiple sclerosis; T cell proliferation;  
 KW suppressor inducer.  
 XX Homo sapiens.  
 XX US5958980-A.  
 PN  
 XX  
 PD 12-JAN-1999.  
 XX  
 PF 06-JUN-1995; 95US-00469540.  
 XX  
 PR 30-MAR-1990; 90US-00502559.  
 PR 28-FEB-1992; 92US-00843752.  
 PR 09-APR-1992; 92US-00863318.  
 PR 09-APR-1993; 93US-00046354.  
 XX (AUTO-) AUTOIMMUNE INC.  
 PA Miller A, Weiner HL, Hafler DA, Al-Sabbagh A;  
 XX DR WPI; 1999-119958/10.  
 XX  
 PT New peptides from immunodominant regions of human myelin basic protein -  
 PT useful as immunosuppressants for treatment of multiple sclerosis.  
 XX  
 PS Claim 1; Col 37; 32pp; English.  
 XX  
 CC This sequence represents a fragment of the human myelin basic protein (MBP). The peptides are immunodominant regions of MBP, and are used as  
 CC the immunosuppressant agents of the invention. The peptides act on the  
 CC response to MBP (or tissues containing it), specifically for treatment of  
 CC multiple sclerosis (MS). They either induce anergy in MBP-reactive T  
 CC cells or actively suppress those cells by inhibiting their proliferation,  
 CC possibly by inducing suppressor T cells. The peptides may also be used to  
 CC detect specific T cells. The MBP fragments do not induce 'global'  
 CC immunosuppression upon prolonged use (increasing the risk of a patient  
 CC developing certain malignancies), will not down regulate normal immune  
 CC responses to pathogenic micro-organisms and are less toxic than drugs  
 CC currently used for the treatment of MS, such as azathioprine (Imuran),  
 XX and cyclosporin A  
 SQ Sequence 18 AA;

Query Match Score 94; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFPKNIVTPRTP 17  
 ID AAY6533 standard; peptide; 18 AA.  
 Db 1 ENPVHFFPKNIVTPRTP 17

RESULT 14  
 AAY6533  
 ID AAY6533 standard; peptide; 18 AA.  
 AC AAY6533;  
 XX  
 DT 21-MAR-2000 (first entry)  
 XX Myelin basic protein fragment MBP(85-102).  
 XX  
 KW Myelin basic protein; MBP; autoimmune mediated demyelinating disease;  
 KW multiple sclerosis; encephalomyelitis; immune response; human.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO957241-A2.  
 PN  
 XX  
 PD 11-NOV-1999.

XX 05-MAY-1999; 99WO-US009930.  
 PP  
 XX 05-MAY-1998; 98US-00073109.  
 PR  
 XX (CORT-) CORIXA CORP.  
 PA  
 XX Arimilli S, Deshpande S;  
 PI  
 XX DR WPI; 2000-072228/05.  
 XX  
 PT Novel peptides for treating autoimmune diseases of central nervous system  
 PT characterized by demyelination.  
 XX  
 PR Example 1; Fig 1A; 57pp; English.  
 XX  
 PS  
 CC The invention provides novel peptides derived from human myelin basic  
 CC protein having an amino acid sequence Phe-X-Lys-Asn-Ile-Val-X-X-X-Thr-X  
 X, where X is any amino acid. The MBP peptides are used in the treatment  
 CC of autoimmune mediated demyelinating disease like multiple sclerosis or  
 CC the murine demyelinating experimental autoimmune encephalomyelitis. The  
 CC therapeutic compositions comprising novel MBP peptides are used for  
 CC inducing oral tolerance or general tolerance. The compositions are used  
 CC to downregulate or eliminate auto-reactive components of the immune system  
 CC and treat auto-reactive demyelinating. T-cell mediated immune response.  
 CC The novel MBP peptides when administered into a subject are useful for  
 CC inhibiting a T-cell mediated immune response against MBP, to treat the T-  
 CC cell mediated immune response which causes a pathological condition of  
 CC the nervous system e.g., multiple sclerosis. Prevention or suppression of  
 CC MHC-restricted immune responses is done without any undesirable side  
 CC effects, such as nonspecific suppression of an individual's overall  
 CC immune response. The MBP peptides provide a safer and more effective  
 CC treatment by selectively suppressing autoimmune responses at the helper  
 CC CD4+ T-cell levels. Sequences AAY6531-553 represent MBP peptides  
 XX  
 SQ Sequence 18 AA;

Query Match Score 94; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFPKNIVTPRTP 17  
 ID AAY6533  
 Db 1 ENPVHFFPKNIVTPRTP 17

RESULT 15  
 AAR32295  
 ID AAR32295 standard; protein; 19 AA.  
 AC AAR32295;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 31-MAY-1993 (first entry)  
 XX  
 Sequence of synthetic peptide MBP 84-102 which corresp. to AAS 84-102 of  
 DB myelin basic protein.  
 XX  
 KW Cytotoxin T lymphocyte response; epitope; antigen.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9301831-A1.  
 XX  
 PD 04-FEB-1993.  
 XX  
 PP 24-JUL-1992; 92WO-US006193.  
 XX  
 PR 25-JUL-1991; 91US-00735069.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Raychaudhuri S, Rastetter WH;

XX  
DR WPI; 1993-058526/07.  
XX

PT New compen. comprising an antigen and a formulation - to induce a  
PT cytotoxic T-lymphocyte response, useful for treating malaria, HIV,  
PT influenza, hepatitis, herpes, cancer, etc.  
XX

PS Disclosure; Page 19; 56pp; English.

XX  
CC Carbone and Bevan demonstrated that cytotoxic T-lymphocyte (CTL) induced  
CC in C57BL/6 mice by EG7-ova transfected, and by cytoplasmically ova-  
CC loaded splenocytes recognise EL4 cells coated with the peptide ova 258-  
CC 276. To determine whether soluble ovalbumin in AF induces similar CTL  
CC responses, spleen cells were prepared from immunised mice and stimulated  
CC in vitro with EG7-ova. The effectors were tested against EL4 cells coated  
CC with the peptide ova 253-276 or with a control peptide derived from  
CC myelin basic protein (MBP 84-102). The results demonstrate that ova-AF  
CC primed CTL with a similar specificity to those primed by transfectants,  
CC or by cytoplasmically loaded ova. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX

SQ Sequence 19 AA:

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFKNTVTPRTP 17  
DB 2 ENPVVHFFKNIVTPRTP 18

Search completed: June 7, 2005, 08:56:41  
Job time : 10.6321 secs

**GenCore version 5.1.6**  
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**OM protein - protein search, using sw model**

**Run on:** June 7, 2005, 08:49:07 ; Search time 2.37824 Seconds  
                   (without alignments)  
                   533.603 Million cell updates/sec

**Title:** US-10-000-439-13  
**Perfect score:** 94  
**Sequence:** 1 ENPVVHFFKNIVTPRTP 17  
**Scoring table:** BLOSUM62  
**Gapop:** 10.0 , Gapext 0.5  
**Searched:** 513545 seqs, 74649364 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

Issued Patents AA:\*

1: /cgnt2\_6/podata/1/1aa/5A\_COMB.pep: \*  
2: /cgnt2\_6/podata/1/1aa/5B\_COMB.pep: \*  
3: /cgnt2\_6/podata/1/1aa/6A\_COMB.pep: \*  
4: /cgnt2\_6/podata/1/1aa/6B\_COMB.pep: \*  
5: /cgnt2\_6/podata/1/1aa/PCTUS\_COMB.pep: \*  
/cgnt2\_6/podata/1/1aa/backfilesls1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query %	Match Length	DB ID	Description
1	94	100.0	17	3 US-09-137-759-3	Sequence 3, Appli
2	94	100.0	17	3 US-09-378-244-3	Sequence 3, Appli
3	94	100.0	18	2 US-08-468-340B-18	Sequence 18, Appli
4	94	100.0	19	2 US-08-640-344-2	Sequence 2, Appli
5	94	100.0	19	2 US-08-468-540B-9	Sequence 9, Appli
6	94	100.0	19	2 US-08-468-540B-17	Sequence 17, Appli
7	94	100.0	19	2 US-08-468-540B-24	Sequence 24, Appli
8	94	100.0	19	3 US-08-297-195-1	Sequence 1, Appli
9	94	100.0	19	3 US-09-024-220-2	Sequence 2, Appli
10	94	100.0	19	3 US-08-960-190A-32	Sequence 32, Appli
11	94	100.0	19	3 US-08-449-728-2	Sequence 2, Appli
12	94	100.0	19	4 US-09-077-028A-15	Sequence 15, Appli
13	94	100.0	19	4 US-09-740-003-2	Sequence 2, Appli
14	94	100.0	20	2 US-08-640-344-1	Sequence 1, Appli
15	94	100.0	20	2 US-08-640-344-3	Sequence 3, Appli
16	94	100.0	20	2 US-08-640-344-4	Sequence 4, Appli
17	94	100.0	20	2 US-08-640-344-5	Sequence 5, Appli
18	94	100.0	20	2 US-08-640-344-6	Sequence 6, Appli
19	94	100.0	20	2 US-08-640-344-7	Sequence 7, Appli
20	94	100.0	20	3 US-08-360-120A-28	Sequence 28, Appli
21	94	100.0	23	1 US-08-787-547-1	Sequence 1, Appli
22	94	100.0	24	2 US-08-480-190-46	Sequence 46, Appli
23	94	100.0	24	2 US-08-488-319-46	Sequence 46, Appli
24	94	100.0	24	4 US-08-475-199A-46	Sequence 46, Appli
25	94	100.0	24	4 US-09-239-043D-201	Sequence 2501, Appli
26	94	100.0	24	4 US-08-077-225A-46	Sequence 46, Appli
27	100.0	513545	513545	PCT-US93-07545-46	Sequence 46, Appli

**ALIGNMENTS**

RESULT 1  
US-09-137-759-3  
; Sequence 3, Application US/09137759  
; Patent No. 6251396  
; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN  
; FILE REFERENCE: 690088.405C1  
; CURRENT APPLICATION NUMBER: US/09/137,759  
; CURRENT FILING DATE: 1998-08-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-137-759-3  
Query Match Similarity 100.0%; Score 94; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.4e-09; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17

RESULT 2  
US-09-378-244-3  
; Sequence 3, Application US/09378244  
; Patent No. 6339670  
; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN  
; FILE REFERENCE: 690088.405C2  
; CURRENT APPLICATION NUMBER: US/09/378,244  
; CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 3  
 LENGTH: 17  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
 US-09-378-244-3

Query Match 100.0%; Score 94; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKIVTPTP 17  
 Db 1 ENPVVHFFKIVTPTP 17

RESULT 3  
 US-08-468-540B-18  
 ; Sequence 18, Application US/08468540B  
 ; Patent No. 5858980  
 GENERAL INFORMATION:  
 APPLICANT: Weiner, Howard  
 APPLICANT: Hafler, David  
 APPLICANT: Miller, Ariel  
 APPLICANT: Al-Sabagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Darby & Darby P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 FILING DATE: 06-JUN-1995  
 APPLICATION NUMBER: US/08/468,540B  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STORELLA ESO, JOHN R.  
 REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 14058-004800  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 US-08-640-344-2

Query Match 100.0%; Score 94; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKIVTPTP 17  
 Db 2 ENPVVHFFKIVTPTP 18

RESULT 5  
 US-08-468-540B-9  
 ; Sequence 9, Application US/08468540B  
 ; Patent No. 5858980  
 GENERAL INFORMATION:  
 APPLICANT: Weiner, Howard  
 APPLICANT: Hafler, David  
 APPLICANT: Miller, Ariel  
 APPLICANT: Al-Sabagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Darby & Darby P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: NY

Query Match 100.0%; Score 94; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKIVTPTP 17

COUNTRY: USA  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,540B  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jacobs, Seth H  
 REGISTRATION NUMBER: 32,140  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-527-7700  
 TELEX:  
 TELEFAX:  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5858980e  
 ;  
 ; US-08-468-540B-9  
 Query Match 100.0%; Score 94; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENPVVHFFKNIKVTPRTP 17  
 Db 2 ENPVVHFFKNIKVTPRTP 18  
 ;  
 ; US-08-468-540B-17  
 Query Match 100.0%; Score 94; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ENPVVHFFKNIKVTPRTP 17  
 Db 2 ENPVVHFFKNIKVTPRTP 18  
 ;  
 ; RESULT 7  
 ; US-08-468-540B-24  
 ; Sequence 24, Application US/08468540B  
 ; Patent No. 5858980  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, Howard  
 ; APPLICANT: Hafler, David  
 ; APPLICANT: Miller, Ariel  
 ; APPLICANT: Al-Sabbagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Darby & Darby P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,540B  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jacobs, Seth H  
 REGISTRATION NUMBER: 32,140  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-527-7700  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5858980e  
 ;  
 ; US-08-468-540B-24  
 Query Match 100.0%; Score 94; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.2e-09; Mismatches 17; Conservative 0; Indels 0; Gaps 0; Qy 1 ENPVHFFKQIVTPRTP 17 Db 2 ENPVHFFKQIVTPRTP 18

RESULT 8  
US-08-297-395-1  
; Sequence 1, Application US/08297395A  
; Patent No. 603947  
; GENERAL INFORMATION:  
; APPLICANT: Howard L. Weiner  
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT FILE REFERENCE: 1010/05721US3 CURRENT APPLICATION NUMBER: US/08/297,395A  
; CURRENT FILING DATE: 1990-03-30  
; EARLIER APPLICATION NUMBER: PCT/US88/02139  
; EARLIER FILING DATE: 1988-06-24  
; EARLIER APPLICATION NUMBER: 08/059,189  
; EARLIER FILING DATE: 1993-05-06  
; EARLIER APPLICATION NUMBER: 07/502,559  
; EARLIER FILING DATE: 1987-06-24  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-08-297-395-1

Query Match 100.0%; Score 94; DB 3; Length 19; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ENPVHFFKQIVTPRTP 17 Db 2 ENPVHFFKQIVTPRTP 18

RESULT 9  
US-09-024-220-2  
; Sequence 2, Application US/09024220  
; Patent No. 6197311  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, Syamal  
; RASITER, William H.  
; BLACK, Amelia  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22311-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960,190A  
; FILING DATE: 29-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 480002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440

RESULT 10  
US-08-960-190A-32  
; Sequence 32, Application US/08960190A  
; Patent No. 6232445  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; APPLICANT: Acevedo, Jorge  
; APPLICANT: Burkhardt, Martin  
; APPLICANT: Jiao, Jin-an  
; APPLICANT: Wong, Bing C.  
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: usa  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960,190A  
; FILING DATE: 29-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 480002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440

; TELEX:  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLogy: linear  
; MOLECULE TYPE: protein  
; US-08-960-190A-32

RESULT 11  
Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVWHFKNIVTPRTP 17  
Db 2 ENPVWHFKNIVTPRTP 18

; GENERAL INFORMATION:  
APPLICANT: SYAMAL RAYCHAUDHURI  
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PS/2 Model 50Z or 55SX-2  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: .ModPerfect (version 5.0)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,728

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/735,069

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 194/160

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLogy: linear  
; US-08-449-728-2

Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVWHFKNIVTPRTP 17  
Db 2 ENPVWHFKNIVTPRTP 18

RESULT 12  
Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVWHFKNIVTPRTP 17  
Db 2 ENPVWHFKNIVTPRTP 18

; GENERAL INFORMATION:  
APPLICANT: IDA STEINBERGER  
APPLICANT: EVELINE BERAUD  
APPLICANT: IRINA MARIANOVSKY  
TITLE OF INVENTION: PSEUDOMONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC FILE REFERENCE: LOREBBEIN=1  
CURRENT APPLICATION NUMBER: US/09/077,028A  
CURRENT FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: ILL16044  
PRIOR FILING DATE: 1995-11-17  
PRIOR APPLICATION NUMBER: ILL15559  
PRIOR FILING DATE: 1995-12-26  
PRIOR APPLICATION NUMBER: PCT/IL96/00151  
PRIOR FILING DATE: 1996-11-17  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO: 15  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
; US-09-077-028A-15

RESULT 13  
Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVWHFKNIVTPRTP 17  
Db 2 ENPVWHFKNIVTPRTP 18

; GENERAL INFORMATION:  
APPLICANT: RAYCHAUDHURI, SYAMAL  
APPLICANT: RASTETTER, WILLIAM H.  
APPLICANT: BLACK, AMELIA  
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
FILE REFERENCE: 37003/275802  
CURRENT APPLICATION NUMBER: US/09/740,003  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/024,220  
PRIOR FILING DATE: 1998-02-17  
PRIOR APPLICATION NUMBER: 08/476,674  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/351,001  
PRIOR FILING DATE: 1994-12-07  
PRIOR APPLICATION NUMBER: 08/919,787  
PRIOR FILING DATE: 1997-08-29  
PRIOR APPLICATION NUMBER: 07/725,069  
PRIOR FILING DATE: 1991-07-25  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 2  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; US-09-740-003-2

Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
           ||||| ||||| |||||  
   2 ENPVVHFFKNIVTPRTP 18

RESULT 14  
 US-08-640-344-1

; Sequence 1, Application US/08640344  
 ; Patent No. 5824315

; GENERAL INFORMATION:

; APPLICANT: NAG, BISHWAJIT

; APPLICANT: MUKRU, PRADEEP

; APPLICANT: DESHPANDE, SHRIRAKANT

; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TWO EMBARCADERO CENTER, 8TH FLOOR

; CITY: SAN FRANCISCO

; STATE: U.S.A.

; COUNTRY: U.S.A.

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/640,344

; FILING DATE: 30-APR-1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: STORELLA ESO., JOHN R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 14058-004800

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-640-344-3

; Query Match Score 94; DB 2; Length 20;

; Best Local Similarity 100.0%; Pred. No. 7.6e-09;

; Matches 17; Conservative 0; Mismatches 0; Indels 0;

; Gaps 0; GapS 0;

; Qy 1 ENPVVHFFKNIVTPRTP 17

; Db 3 ENPVVHFFKNIVTPRTP 19

Query Match Score 94; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0; GapS 0;  
 Qy 1 ENPVVHFFKNIVTPRTP 17  
 Db 3 ENPVVHFFKNIVTPRTP 19

Search completed: June 7, 2005, 09:04:02  
 Job time : 3.37824 secs

RESULT 15  
 US-08-640-344-3

; Sequence 3, Application US/08640344  
 ; GENERAL INFORMATION:  
 ; Patient No. 5824315

; APPLICANT: NAG, BISHWAJIT

; APPLICANT: MUKRU, PRADEEP

; APPLICANT: DESHPANDE, SHRIRAKANT

; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND & CREW LLP

; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

; CITY: SAN FRANCISCO

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### OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 38 Seconds  
 (without alignments)  
 43.044 Million cell updates/sec

Title: US-10-000-439-13  
 Perfect score: 94  
 Sequence: 1 ENPVVHFKNIVTPRTP 17  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

### Database :

1: PIR:79:  
 2: pir1:  
 3: pir2:  
 4: pir3:  
 4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

### ALIGNMENTS

#### RESULT 1

S12904 protein kinase (EC 2.7.1.37) - starfish (*Piaster ochraceus*)

C;Species: *Piaster ochraceus*  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S12904  
 R;Sanghera, J.S.; Bebbertold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
 FEBs Lett. 273, 223-226, 1990

A;Title: Identification of the sites in myelin basic protein that are phosphorylated by n

A;Reference number: S12904; MUID:91032186; PMID:1699809  
 A;Accession: S12904

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <SIN>

A;Cross-references: UNIPROT:Q7M3M4  
 C;Keywords: phosphotransferase

Query Match Similarity 45.7%; Score 43; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.41; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 NIVTPRTP 17

Qy ||||| B

#### RESULT 2

A54348 N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: A54348  
 R;Shilatard, A.; Cummings, R.D.

Biochemistry 33, 4273-4282, 1994

A;Title: Purification and characterization of N-acetylglucosamine-6-sulfatase from

A;Reference number: A54348; MUID:94206936; PMID:8155645

A;Accession: A54348

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SII>

C;Keywords: Bulfuric ester hydrolase

Query Match Similarity 25.5%; Score 24; DB 2; Length 11;

Best Local Similarity 62.5%; Pred. No. 5.5e-02; Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 4 FFMIXTP 11

Qy ||||| B

### RESULT 3

annexin VI homolog  
 L-ascorbate peroxidase  
 endoglycosidase  
 seed protein wa-18  
 trichorizin I - fu  
 trichorizin III -  
 neural cell adhesin  
 neuregulin bovi  
 calreticulin, hepa  
 cell surface glyco  
 xylan 1,4-beta-D-xyl  
 formate dehydrogen  
 disintegrinase - M  
 Pax QNR, long form  
 calreticulin, uter  
 pseudogerminal - whe

SO3405 hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)  
 C;Species: Alcaligenes eutrophus  
 C;Accession: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Sep-1998  
 C;Title: Immunological comparison of subunits isolated from various hydrogenases of aerobically respiration  
 R;Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.  
 Biochim. Biophys. Acta 995, 1-9, 1989  
 A;Reference number: SO3404; MUID:8916625; PMID:2493816  
 A;Molecule type: protein  
 A;Residues: 1-16 <LOR>  
 A;Experimental source: strain R16, DMS 541  
 C;Superfamily: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein; nif  
 C;Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein; nif  
 Query Match Best Local Similarity 25.5%; Score 24; DB 2; Length 16;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 14 PRTP 17  
 Db 5 PRTP 8

RESULT 4

A59046 alpha-conotoxin MII - cone shell (Conus magus)  
 C;Species: Conus magus (magus cone)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C;Accession: A59046  
 R;Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.  
 J. Biol. Chem. 271, 7522-7528, 1996  
 A;Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptor  
 A;Accession: A59046  
 A;Status: preliminary  
 A;Residues: 1-16 <CAR>  
 A;Cross-references: UNIPROT:P56636  
 C;Superfamily: alpha-conotoxin  
 C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotransmitter  
 F;1-16/Product: alpha-conotoxin MII #status experimental <MTS>  
 F;2-8,3-16/Diubiquitin bonds: #status experimental  
 F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match Best Local Similarity 25.5%; Score 24; DB 2; Length 16;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NPYVWH 6  
 Db 5 NPYVCH 9

RESULT 5

S55696 phosphoenolpyruvate carboxykinase - Trypanosoma brucei  
 C;Species: Trypanosoma brucei  
 C;Accession: S55696  
 R;Hunt, M.; Koehler, P.  
 Biochim. Biophys. Acta 1249, 15-22, 1995  
 A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Trypanosoma brucei  
 A;Reference number: S55696; MUID:95284106; PMID:7766679  
 A;Accession: S55696  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <HN>  
 A;Cross-references: UNIPROT:Q7M3S5

Query Match Best Local Similarity 24.5%; Score 23; DB 2; Length 9;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PVVHFKNI 11  
 Db 2 PIH-KNL 8

RESULT 6

PH1628 Ig H chain V-D-J region (clone B-Less 151) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1628  
 R;Levinson, D.A.; Campod-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-339, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1628  
 A;Molecule type: DNA  
 A;Residues: 1-14 <LBV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match Best Local Similarity 24.5%; Score 23; DB 2; Length 14;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HFFPKNIV 12  
 Db 4 HYYSNLL 10

RESULT 7

S65520 phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)  
 C;Contains: muscarinic acetylcholine receptor inhibitor  
 C;Species: Naja naja sputatrix (Malayan spitting cobra)  
 C;Accession: S65520  
 C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
 R;Myoshi, S.; Tu, A.T.  
 Arch. Biochem. Biophys. 328, 17-25, 1996  
 A;Title: Phospholipase A(2) from Naja naja sputatrix venom is a muscarinic acetylcholine receptor number: S65520; MUID:9619575; PMID:8638927  
 A;Accession: S65520  
 A;Molecule type: protein  
 A;Residues: 1-16 <MT>  
 A;Cross-references: UNIPROT:Q10756  
 C;Superfamily: phospholipase A2  
 C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; presenilin

Query Match Best Local Similarity 24.5%; Score 23; DB 2; Length 16;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 8 FKNIVTPRT 17  
 Db 5 FKNNIQCTVP 14

RESULT 8

S58355 neuropeptide FFRFamide - blue mussel  
 N;Alternate names: FMRFamide-related decapeptide; Mytilus FFRFamide  
 C;Species: Mytilus edulis (blue mussel)  
 C;Accession: 20-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
 C;Accession: A58355  
 R;Fujisawa, Y.; Ikeda, T.; Nomoto, K.; Yasuda-Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Comp. Biochem. Physiol. C 102, 91-95, 1992  
 A;Title: The FMRFamide-related decapeptide of Mytilus contains a D-amino acid residue.  
 A;Reference number: A58355; MUID:93047882; PMID:1358533  
 A;Accession: A58355  
 A;Molecule type: protein  
 A;Residues: 1-10 <FOU>

A;Cross-references: UNIPROT:P42560  
A;Experimental source: anterior bursus retractor muscle  
C;Keywords: amidated carboxyl end; neuropeptide  
F;1/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.4%; Score 22; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03; Mismatches 3; Conservative 1; Indels 0; Gaps 0; Matches 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HFFK 9  
Db 6 HFFR 9

RESULT 9

S42620 aggrecan - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998  
C;Accession: S42620  
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.  
Matrix Biol. 14, 171-179, 1994  
A;Title: Aggrecan in bovine tendon.  
A;Reference number: S42620; MUID:94340214; PMID:7520336  
A;Accession: S42620  
A;Molecule type: protein  
A;Residues: 1-7 <VOG>  
A;Experimental source: flexor tendon  
C;Keywords: cartilage

Query Match 22.3%; Score 21; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05; Mismatches 4; Conservative 1; Indels 0; Gaps 0; Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 11 IVTPR 15  
Db 3 IVSPR 7

RESULT 10

S62641 porphobilinogen synthase (EC 4.2.1.24) - green alga (Scenedesmus obliquus) (fragment)  
C;Species: Scenedesmus obliquus  
C;Accession: S62641  
R;Stolz, M.; Doermann, D.  
Eur. J. Biochem. 236, 600-608, 1995  
A;Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a C;Species: Scenedesmus obliquus  
C;Accession: S62641  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S62641  
R;Stolz, M.; Doermann, D.  
Eur. J. Biochem. 236, 600-608, 1995  
A;Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a C;Species: Scenedesmus obliquus  
C;Accession: S62641; MUID:96195670; PMID:8612634  
A;Accession: S62641  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <STO>  
A;Cross-references: UNIPROT:Q9SB81  
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 22.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.6e+03; Mismatches 4; Conservative 1; Indels 0; Gaps 0; Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 11 IVTPR 15  
Db 11 IVSPR 15

RESULT 11

A43977 FMRFanide-like protein - tobacco hornworm  
C;Species: Manduca sexta (tobacco hornworm)  
C;Accession: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: A43977

R;Kingan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.; Peptides 11, 849-856, 1990  
A;Title: A new peptide in the FMRFanide family isolated from the CNS of the hawkmoth, Mariposa  
A;Reference number: A43977; MUID:91045350; PMID:2235684  
A;Accession: A43977  
A;Molecule type: protein  
A;Residues: 1-10 <KIN>  
A;Cross-references: UNIPROT:P18523  
C;Species: amidated carboxyl end; neuropeptide; pyroglutamic acid (Gln) #status experimental  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;1/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 21.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.4e+03; Mismatches 4; Conservative 0; Indels 0; Gaps 0; Matches 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VHFFF 8  
Db 3 VHFSF 7

RESULT 12

PH1620 Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1620  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1620; MUID:9301609; PMID:8315387  
A;Accession: PH1620  
A;Molecule type: DNA  
A;Residues: 1-13 <LAV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 21.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03; Mismatches 4; Conservative 0; Indels 0; Gaps 0; Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 11 IVTP 14  
Db 6 IVTP 9

RESULT 13

PC2369 unidentified 85K protein [imported] - *Bacillus cereus* (strain ts-4) (fragment)  
C;Species: *Bacillus cereus*  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: PC2369  
R;Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.  
Biosci. Biotechnol. Biochem. 59, 231-235, 1995  
A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*  
A;Accession: PC2369  
A;Reference number: PC2369; MUID:95218265; PMID:7766022  
A;Accession: PC2369  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <MAS>  
A;Cross-references: UNIPROT:Q7M044

Query Match 21.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.2e+03; Mismatches 4; Conservative 0; Indels 0; Gaps 0; Matches 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ENPVH 7  
Db 7 ENPKWF 13

RESULT 14

S62374

alpha-1-antichymotrypsin - human (Fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S62374  
 R;Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Teuda, T.;  
 Eur. J. Biochem. 235, 821-827, 1996  
 A;Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia-  
 A;Reference number: S62374; MUID: 96184564; PMID: 8654434  
 A;Accession: S62374  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-14 <TSU>  
 A;Cross-references: UNIPROT:Q9UNU9; UNIPROT:Q96DW8; UNIPROT:QBN177

Query Match 21.3%; Score 20; DB 2; Length 14;  
 Best Local Similarity 18.2%; Pred. No. 3.5e+03;  
 Matchers 2; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Qy 5 VHFPKKNIVPR 15  
 Db 2 IFFMSKVTPK 12

RESULT 15  
A35417  
28K Serine proteinase homolog - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 1-Jan-1991 #Sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C;Accession: A35417  
R.Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambardini, A.G.  
Biochem. Biophys. Res. Commun. 170, 769-774, 1990  
A;Title: Co-purification of proteases with basic fibroblast growth factor (FGF).  
A;Reference number: A35417; MUID:90343797; PMID:2200404  
A;Accession: A35417  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <HOA>  
A;Cross-references: UNIPROT:Q7M3G3

Query Match	21.3%	Score 20;	DB 2;	Length 15;
Best Local Similarity	66.7%	Pred. No. 3.8e+03;	Mismatches 2;	Indels 0;
Matches	4;	Conservative		Gaps 0;
Oy	9	KNTVTP 14		
Db	10	KGYVTP 15	.	

Search completed: June 7, 2005, 09:37:15  
Job time : 40 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.														
<b>OM protein - protein search, using sw model</b>														
Run on: June 7, 2005, 09:33:36 ; Search time 165 Seconds (without alignments) 52.760 Million cell updates/sec														
Title: US-10-000-439-13 Perfect score: 94 Sequence: 1 ENPVVHFFKNIIVPRTP 17														
<b>Scoring table:</b> BLOSUM62 Gapop 10.0 , Gapext 0.5														
<b>Searched:</b> 1612378 sqqs, 512079187 residues														
Total number of hits satisfying chosen parameters: 8390														
Minimum DB seq length: 0 Maximum DB seq length: 17														
<b>Post-processing:</b> Minimum Match 0% Maximum Match 100% Listing first 45 summaries														
<b>Database :</b> UniProt 03:*														
1: uniprot_sprot:*														
2: uniprot_trembl:*														
<b>Pred.</b> No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.														
<b>SUMMARIES</b>														
Result No.	Score	Query Length	DB ID	Description										
1	43	45.7	14 2	Q7M3M4										
2	30	31.9	15 2	Q9BX4X	Q7M3M4 pisaster oc									
3	30	31.9	15 2	Q6LCH6	Q9Bxx4 homo sapien									
4	28	29.8	16 2	Q8YNS2	Q6Lch6 mus musculus									
5	27	28.7	15 2	Q69J42	Q8YNS2 escherichia									
6	25	26.6	10 2	Q7NSN9	Q69J42 streptococc									
7	25	26.6	12 2	QBYY9	Q7NSN9 plasma									
8	25	26.6	12 2	Q6UC79	QBYy9 homo sapien									
9	25	26.6	12 2	Q7IBQ0	Q6UC79 solenodon p									
10	25	26.6	12 2	Q7IBQ1	Q7IBQ0 cynocephalus									
11	25	26.6	12 2	Q9BR4	Q7IBQ1 urogale eve									
12	25	26.6	12 2	Q9BR5	Q9BR4 manis pent									
13	25	26.6	12 2	Q9BR6	Q9BR5 ursus arcto									
14	25	26.6	12 2	Q9BR7	Q9BR6 canis famili									
15	25	26.6	12 2	Q9BR8	Q9BR7 panthera on									
16	25	26.6	12 2	Q9BR9	Q9BR8 leopardus p									
17	25	26.6	12 2	Q9BS0	Q9BR9 felis silve									
18	25	26.6	12 2	Q9BS1	Q9BS0 tapirus ind									
19	25	26.6	12 2	Q9BS2	Q9BS1 ceratotheri									
20	25	26.6	12 2	Q9BS3	Q9BS2 equus cabal									
21	25	26.6	12 2	Q9BS4	Q9BS3 okapia john									
22	25	26.6	12 2	Q9BR5	Q9BS4 sus scrofa									
23	25	26.6	12 2	Q9BS6	Q9BR5 tragelaphus									
24	25	26.6	12 2	Q9BS7	Q9BS6 lama glama									
25	26.6	12 2	Q9BS8	Q9BS7 hippopotamu										
26	26.6	12 2	Q9BS9	Q9BS8 turtonops tr										
27	26.6	12 2	Q9BT0	Q9BS9 megatheria n										
28	26.6	12 2	Q9BT1	Q9BT0 nyctereis th										
29	26.6	12 2	Q9BT2	Q9BT1 rousettus l										
30	26.6	12 2	Q9BT3	Q9BT2 pteropus gi										
31	26.6	12 2	Q9BT4	Q9BT3 artibeus ja										
<b>ALIGNMENTS</b>														
<b>RESULT 1</b>														
ID	Q7M3M4	PRELIMINARY;			PRT;	14 AA.								
AC	Q7M3M4;													
DT	01-MAR-2004 (TREMBLEL 26, Created)													
DT	01-MAR-2004 (TREMBLEL 26, Last sequence update)													
DT	01-MAR-2004 (TREMBLEL 26, Last annotation update)													
DE	Protein kinase (EC 2.7.1.37).													
OS	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Anterozoa; Asterioidea; Forcipulatacea; Forcipulata; Asteroideae; Pisaster.													
OC	NCBI_TaxID=7612;													
RN	[1]													
RP	SEQUENCE.													
RX	MEDLINE=91032186; PubMed=1699809; DOI=10.1016/0014-5793(90)81090-B;													
RA	Sanghera J.S., Heberstadt R., Morrison H.D., Bures E.J., Pelech S.L.;													
RT	"Identification of the sites in myelin basic protein that are phosphorylated by meiosis-activated protein kinase p44(mpk).";													
RL	FEMS Lett. 273:223-226(1990).													
DR	GO; GO:0004672; P:protein kinase activity; IEA.													
DR	GO; GO:002904; S11904.													
DR	SEQUENCE.													
SQ	SEQUENCE 14 AA; 1492 MW; 908736837308171 CRC64;													
<b>RESULT 2</b>														
ID	Q9BXX4	PRELIMINARY;			PRT;	15 AA.								
AC	Q9BXX4;													
DT	01-JUN-2001 (TREMBLEL 17, Created)													
DT	01-JUN-2001 (TREMBLEL 17, Last sequence update)													
DT	05-JUL-2004 (TREMBLEL 27, Last annotation update)													
DE	Transcription factor PAX 5 (PAX5) (B-cell specific transcription factor) (Fragment).													
GN	Name=PAX5; Synonyms=PAX-5;													
OS	Homo sapiens (Human).													
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.													
OX	NCBI_TaxID=9606;													
RN	[1]													
RP	SEQUENCE FROM N.A.													
RA	Hirabayashi Y., Rahman M., Sasaki T.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.													
RP	[2]													
RP	SEQUENCE FROM N.A.													
RP	MEDLINE=213-4098; PubMed=11460166; DOI=10.1038/35055588;													
RX	PASQUALUCCI L., Neumeister P., Goossens T., Nanjangud G., RA													

RA	Chaganti R.S.K., Kuppers R., Dalla-Favera R.; B-cell diffuse large-cell lymphomas";	"Hypermutation of multiple proto-oncogenes in B-cell diffuse large-cell lymphomas";	Enterobacteriaceae; Escherichia.
RT	Nature 412:341-346 (2001).	[1]	OX NCBI_TaxID:562;
RL			RN [3]
RP	SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.
RN	[3]		RA STRAIN=413_89-1;
RA	MEDLINE=96234102; PubMed=8650231; DOI=10.1073/pnas.93.12.6129; Buselinger M., Klix N., Pfeffer P., Grainger P.G., Kozmik Z.; "Deregulation of Pax-5 by translocation of the Emu enhancer of the IgH locus adjacent to two alternative Pax-5 promoters in a diffuse large-cell lymphoma.;"		RA Benkel P., Chakraborty T.; Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RT	Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134 (1996).		DR EMBL; AJ277443; CAC81838.1; "-.
RL	DR EMBL; AF268279; AAC25371.1; "-.		DR EMBL; AF268790; AAC25371.1; "-.
DR	EMBL; AF268335; AAB16832.1; "-.		FT NON TER 16 16
FT	SEQUENCE 15 AA; 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;		FT NON TER 16 16
SQ	NON TER 15 AA; 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;		FT NON TER 16 16
Query Match Similarity 31.9%; Score 30; DB 2; Length 15; Matches 6; Conservative 0; Pred. No. 6.6e+02; Indels 0; Gaps 0;			FT NON TER 16 16
Qy	9 KNIVPVRT 16		FT NON TER 16 16
Db	5 KNYPTPRT 12		FT NON TER 16 16
RESULT 3			FT NON TER 16 16
ID	Q6LCH6 PRELIMINARY; PRT; 15 AA.		FT NON TER 16 16
AC	Q6LCH6;		FT NON TER 16 16
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		FT NON TER 16 16
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		FT NON TER 16 16
DE	B-cell specific transcription factor (Fragment).		FT NON TER 16 16
GN	Name=PAX-5;		FT NON TER 16 16
OS	Mus musculus (Mouse).		FT NON TER 16 16
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.		FT NON TER 16 16
OX	NCBI_TaxID=10890;		FT NON TER 16 16
RN	[1]		FT NON TER 16 16
RP	SEQUENCE FROM N.A.		FT NON TER 16 16
RC	STRAIN=129/SV;		FT NON TER 16 16
RX	MEDLINE=96234102; PubMed=8650231; DOI=10.1073/pnas.93.12.6129; Busslinger M., Klix N., Preffer P., Graminger P.G., Kozmik Z.; "Deregulation of Pax-5 by translocation of the Emu enhancer of the IgH locus adjacent to two alternative Pax-5 promoters in a diffuse large-cell lymphoma.;"		FT NON TER 16 16
RT	Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134 (1996).		FT NON TER 16 16
DR	EMBL; U56837; AAB16034.1; "-.		FT NON TER 16 16
FT	NON TER 15 AA; 1835 MW; 3F95ABE3FB3F7A8E CRC64;		FT NON TER 16 16
SQ	SEQUENCE 15 AA; 15 AA; 1835 MW; 3F95ABE3FB3F7A8E CRC64;		FT NON TER 16 16
Query Match Similarity 31.9%; Score 30; DB 2; Length 15; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			FT NON TER 16 16
Qy	9 KNIVPVRT 16		FT NON TER 16 16
Db	5 KNYPTPRT 12		FT NON TER 16 16
RESULT 4			FT NON TER 16 16
ID	Q8VNS8 PRELIMINARY; PRT; 16 AA.		FT NON TER 16 16
AC	Q8VNS8;		FT NON TER 16 16
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		FT NON TER 16 16
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		FT NON TER 16 16
DE	CadC protein (Fragment).		FT NON TER 16 16
GN	Name=CadC; Escherichia coli.		FT NON TER 16 16
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		FT NON TER 16 16
OX			FT NON TER 16 16
RN			FT NON TER 16 16
RA	SEQUENCE FROM N.A.		FT NON TER 16 16
RT	PubMed=12368865; DOI=10.1038/nature01099; Carlton J.M., Angulo S.V., Sun B.B., Selenig T.W., Pertea M., Salva J.C., Ermolaeva M.D., Allen J.E., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,		FT NON TER 16 16
RL	Carleton J.M., Angulo S.V., Sun B.B., Selenig T.W., Pertea M., Salva J.C., Ermolaeva M.D., Allen J.E., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,		FT NON TER 16 16
RP	SEQUENCE FROM N.A.		FT NON TER 16 16
RN			FT NON TER 16 16
RA	Strain=17XNL;		FT NON TER 16 16
RT	PubMed=12368865; DOI=10.1038/nature01099; Carlton J.M., Angulo S.V., Sun B.B., Selenig T.W., Pertea M., Salva J.C., Ermolaeva M.D., Allen J.E., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,		FT NON TER 16 16
RL	Carleton J.M., Angulo S.V., Sun B.B., Selenig T.W., Pertea M., Salva J.C., Ermolaeva M.D., Allen J.E., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,		FT NON TER 16 16
RP	SEQUENCE FROM N.A.		FT NON TER 16 16
RN			FT NON TER 16 16
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RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V., RP  
 RA Cho J.K., Quackenbush J., Sedgah M., Shababi A., Cumming L.M., SEQUENCE FROM N.A.  
 RA Flores L., Yates F.R., III, Reine J.D., Sinden R.E., Harris M.A., RX PubMed=15190349; DOI=10.1038/nature02597;  
 RA Cunningham D.A., Prosser P.R., Bergman L.W., Vaidya A.B., Roca A.L., Bar-Gal G.K., Bzirk E., Helgen K.M., Maria R.,  
 RA van Lin J.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Springer M.S., O'Brien S.J., Murphy W.J.;  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., RT "Merozoic origin for West Indian insectivores.";  
 RA Carucci D.J.; RFL Nature 422:649-651(2004).  
 RA "Genome sequence and comparative analysis of the model rodent malaria RLL  
 RT parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC - CAUTION: The sequence shown here is derived from an RLT  
 CC EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is RLS Nature 422:649-651(2004).  
 CC preliminary data.  
 DR EMBL: AA0100088; EAA22681.1; -. RDR  
 KW Hypothetical protein. RDR  
 PT NON TER RDR  
 SQ SEQUENCE 10 AA; 1209 MW; 3F8986573B42C047 CRC64;  
 Query Match 26.6%; Score 25; DB 2; Length 10; RDR  
 Best Local Similarity 42.9%; Pred. No. 3.e+03; Gaps 0; Gaps 0; RDR  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0; RDR  
 Qy 2 NPVHFF 8 RDR  
 Db 2 NPIVLY 8 RDR  
 RESULT 7 RDR  
 ID QBYY9 PRELIMINARY; PRT; 12 AA. RDR  
 AC QBYY9; RDR  
 DT 01-JUN-2001 (TREMBLrel. 17, Created) RDR  
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update) RDR  
 DE Amyloid beta protein (Fragment). RDR  
 GN Name=APP; RDR  
 OS Homo sapiens (Human). RDR  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; RDR  
 OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus. RDR  
 RX MBDLINE=21082002; PubMed=11214319; DOI=10.1088/33054550; RDR  
 RA O'Brien S.J.; RDR  
 RT Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RDR  
 RN [1] RDR  
 RP SEQUENCE FROM N.A. RDR  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A., RDR  
 RA Bzik E., Murphy W.J., Springer M.S., O'Brien S.J.; RDR  
 RT "Molecular phylogenetics and the origins of placental mammals."; RDR  
 RL Nature 409:614-618(2001). RDR  
 DR EMBL: AY011354; RAG7389.1; -. RDR  
 PT NON TER 1 1 RDR  
 SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64; RDR  
 Query Match 26.6%; Score 25; DB 2; Length 12; RDR  
 Best Local Similarity 40.0%; Pred. No. 3.7e+03; Gaps 0; Gaps 0; RDR  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0; RDR  
 Qy 2 NPVHFFKNI 11 RDR  
 Db 1 NPTYKFFEQM 10 RDR  
 RESULT 8 RDR  
 ID Q6JC79 PRELIMINARY; PRT; 12 AA. RDR  
 AC Q6JC79; RDR  
 DT 05-JUL-2004 (TREMBLrel. 27, Created) RDR  
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update) RDR  
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update) RDR  
 DE APP (Fragment). RDR  
 OS Uroptile everetti. RDR  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; RDR  
 OC Mammalia; Buterria; Scandentia; Tupaiidae; Urogale. RDR  
 OC NCBI\_TaxID=192726; RDR  
 RN [1] RDR  
 RP SEQUENCE FROM N.A. RDR  
 RA Bzik E., Murphy W.J., Springer M.S., O'Brien S.J.; RDR  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDJB databases. RDR  
 DR EMBL: AF535039; AAQ10583.1; -. RDR  
 PT NON TER 1 1 RDR  
 SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64; RDR  
 Query Match 26.6%; Score 25; DB 2; Length 12; RDR  
 Best Local Similarity 40.0%; Pred. No. 3.7e+03; Gaps 0; Gaps 0; RDR  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0; RDR  
 Qy 2 NPVHFFKNI 11 RDR

Db      1 ||| : :      1 NPTYKFFEQM 10

RESULT 11

Q9BFR4      PRELIMINARY;      PRT;      12 AA.

ID Q9BFR4  
Q9BFR4;      DT 01-JUN-2001 (TREMBREL. 17, Created)  
DT 01-JUN-2001 (TREMBREL. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)

DE Amyloid beta protein (Fragment).

GN Name=APP;  
Canis familiaris (Dog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TAXID=9615;

RP SEQUENCE FROM N.A.

RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;  
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY011374; AAC47409.1; -.

FT NON\_TER 1 1  
SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match      26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVWHFPKNI 11  
Db 1 NPTYKFFEQM 10

RESULT 12

Q9BFR5      PRELIMINARY;      PRT;      12 AA.

ID Q9BFR5  
AC Q9BFR5;      DT 01-JUN-2001 (TREMBREL. 17, Created)  
DT 01-JUN-2001 (TREMBREL. 17, Last sequence update)

DE Amyloid beta protein (Fragment).

GN Name=APP;  
Panthera onca (Jaguar).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.  
OX NCBI\_TAXID=9690;

RP SEQUENCE FROM N.A.

RX MEDLINE=1082082; PubMed=11214319; DOI=10.1038/35054550;  
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY011374; AAC47409.1; -.

FT NON\_TER 1 1  
SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match      26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVWHFPKNI 11  
Db 1 NPTYKFFEQM 10

RESULT 13

Q9BFR6      PRELIMINARY;      PRT;      12 AA.

Db 1 NPTYKFFEQM 10

RESULT 14

Q9BFR7      PRELIMINARY;      PRT;      12 AA.

ID Q9BFR7  
AC Q9BFR7;      DT 01-JUN-2001 (TREMBREL. 17, Created)  
DT 01-JUN-2001 (TREMBREL. 17, Last sequence update)

DE Amyloid beta protein (Fragment).

GN Name=APP;  
Leopardus pardalis (Ocelot).  
OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.  
OX NCBI\_TaxID=32538;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082002; PubMed=11214319; DOI=10.1038/35054550;  
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:611-618(2001).  
DR EMBL; AY011370; AACG7405.1; -.  
FT NON\_TER 1  
SQ 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
Query Match 26.6%; Score 25; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 NPVWHFKNTI 11  
| | : :  
Db 1 NPTYKPFPEQM 10

Search completed: June 7, 2005, 09:36:30  
Job time : 166 secs

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GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time: 67 Seconds  
 (without alignments)  
 98.133 Million cell updates/sec

Title: US-10-000-439-13  
 Perfect score: 94  
 Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BL0SUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 664154

Minimum DB seq length: 0  
 Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:  
 1: geneseqp1980s:  
 2: geneseqp1990s:  
 3: geneseqp2000s:  
 4: geneseqp2001s:  
 5: geneseqp2002s:  
 6: geneseqp2003as:  
 7: geneseqp2003bs:  
 8: geneseqp2004bs:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	94	100.0	17	3 AAY69395
2	94	100.0	17	5 AAO20308
3	94	100.0	17	5 AAE26359
4	94	100.0	17	5 AAE23935
5	94	100.0	17	6 AEP97941
6	94	100.0	17	6 ABR56063
7	94	100.0	17	6 AAO19672
8	94	100.0	17	7 ADB50773
9	94	100.0	17	8 ADK67704
10	94	100.0	17	8 ADL18291
11	89	94.7	17	2 ARR4116
12	89	94.7	17	2 ARR95360
13	89	94.7	17	2 AAW73601
14	89	94.7	17	3 AAY66534
15	87	92.6	17	2 ARR44118
16	87	92.6	17	2 ARR95354
17	87	92.6	17	2 AAW72353
18	87	92.6	17	2 AAW73602
19	83	88.3	16	2 AAR44117
20	83	88.3	16	2 AAR95361
21	83	88.3	16	3 AAY66535
22	83	88.3	16	5 AAE23936
23	82	87.2	15	2 AAR4120
24	82	87.2	15	2 AAW05498
25	82	87.2	15	2 AAW04856

## ALIGNMENTS

RESULT 1	
ID	AAY69395
XX	
AC	AAY69395;
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	Peptide derived from a human myelin basic protein.
XX	
KW	Human; myelin basic protein; oligodendroglial cell; Th2 immune response; Th2-type cytokine; analogue; multiple sclerosis.
KW	
OS	Synthetic.
XX	
OS	Homo sapiens.
PN	W0200011027-A1.
XX	
PD	02-MAR-2000.
XX	
PP	19-AUG-1999; 99WO-US019033.
PR	20-AUG-1998; 98US-00137759.
XX	
(NOVS )	NOVARTIS AG.
PA	(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
XX	
PI	Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;
XX	
DR	MPI; 2000-224661/19.
XX	
PT	Inducing a Th2 immune response and a persistent systemic immune response to myelin basic protein, MBP, or a peptide analog of MBP for use in treating multiple sclerosis, by administering compositions comprising peptide analogs of MBP.
PT	
PT	The present sequence represents a peptide derived from human myelin basic protein. Myelin basic protein is found in the cytoplasm of human oligodendroglial cells. Peptide analogue derived from the present sequence are administered to a patient in need to induce a Th2 immune response (i.e. production of T cells producing one or more Th2-type cytokines) and/or a persistent systemic immune response to myelin basic protein. These peptide analogues are at least seven amino acids long derived from residues 83-99 of human myelin basic protein and altered from the native sequence at least at positions 91, 95 or 97. The peptide

CC analogs are especially useful in the treatment of multiple sclerosis  
 XX SQ Sequence 17 AA;

Query Match	100.0%	Score	94;	DB	3;	Length	17;
Best Local Similarity	100.0%	Pred. No.	6.1e-09;				
Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	ENPVVHFFKQIVTPRPP	17				
Db	1	ENPVVHFFKQIVTPRPP	17				

RESULT 2  
 AAO20308  
 ID AAO20308 standard; peptide; 17 AA.

XX AC AAO20308;

XX DT 31-MAY-2002 (first entry)

DE Myelin basic protein (MBP) apitope peptide region 83-99.

XX KW MBP; myelin basic protein; apitope; antiasthmatic; tolerogenic peptide; dermatological; antiallergic; neuroprotective; antithyroid; antidiabetic; class I; vasotropic; antiinflammatory; immunosuppressive; antidiabetic; class I; major histocompatibility complex; MHC; class II; autoimmune thyroiditis; KW hypersensitivity disorder; antigen; allergy; extrinsic asthma; urticaria; autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis; autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis; systemic sclerosis; polymyositis; diabetes; transplant rejection; antiviral CD8+.

XX OS Unidentified.

XX PN WO200216410-A2.

XX PD 28-FEB-2002.

XX PR 17-AUG-2001; 2001WO-GB003702.

XX PR 21-AUG-2000; 2000GB-00020618.

XX PR 14-JUN-2001; 2001GB-00014547.

XX PR (UYBR-) UNIV BRISTOL.

XX PI Wraith DC, Anderton SM, Mazza G, Ponsonby M, Streeter RB;

XX DR WPI; 2002-292056/33.

XX PT Selecting tolerogenic peptide useful for treating autoimmune diseases e.g. multiple sclerosis, involves selecting peptide which binds major histocompatibility complex class I or II molecule without further PT processing.

XX PS Claim 12; Page 28; 55pp; English.

CC The invention relates to a method for selecting a tolerogenic peptide, comprising selecting a peptide which is capable of binding to a major histocompatibility complex (MHC) class I or II molecule without further processing. The peptides of the invention are useful for preventing a disease such as hypersensitivity disorder, and also for treating and/or preventing a disease in a subject. The method involves identifying an antigen for the disease, identifying an apitope (antigen processing independent epitope) for the antigen, and administering the apitope to the subject. The peptides of the invention are also useful for treating allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis, urticaria, autoimmune diseases such as multiple sclerosis, sarcoidosis, autoimmune thyroiditis, Grave's disease, systemic sclerosis, hemolytic anaemia, polyposis, diabetes, etc., and transplant rejection. The peptides are also useful for modifying antiviral CD8+ responses in a tolerogenic fashion. This sequence represents an apitope of the invention of peptide region 83-99 of Myelin basic protein (MBP).

XX SQ Sequence 17 AA;

Query Match	100.0%	Score	94;	DB	5;	Length	17;
Best Local Similarity	100.0%	Pred. No.	6.1e-09;				
Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	ENPVVHFFKQIVTPRPP	17				
Db	1	ENPVVHFFKQIVTPRPP	17				

RESULT 3  
 AAE26359  
 ID AAE26359 standard; peptide; 17 AA.

XX AC AAE26359;

XX DT 13-DEC-2002 (first entry)

DE Peptide related to myelin basic protein.

XX KW Th2 immune response; myelin basic protein; MBP; vaccine; MS; multiple sclerosis; anti-sclerotic.

XX OS Unidentified.

XX PN US6379670-B1.

XX PD 30-APR-2002.

XX PP 19-AUG-1999; 99US-00378244.

XX PR 18-NOV-1994; 94US-00342408.

XX PR 20-AUG-1998; 98US-00137759.

XX PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX PA (NOVS-) NOVARTIS AG.

XX PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;

XX DR WPI; 2002-461895/49.

XX PT Inducing Th2 immune responses to Myelin Basic Protein (MBP) by PT administering the MBP peptide analog CGP 77116, useful for treating PT Multiple Sclerosis.

XX PS Disclosure; Col 35-36; 49pp; English.

CC The present invention relates to a novel method for inducing Th2 immune responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a patient. The method involves administering a composition comprising the MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for treating multiple sclerosis (MS). Sequences of the invention are also used as vaccines. The present sequence is a peptide related to human MBP.

XX SQ Sequence 17 AA;

Query Match	100.0%	Score	94;	DB	5;	Length	17;
Best Local Similarity	100.0%	Pred. No.	6.1e-09;				
Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	ENPVVHFFKQIVTPRPP	17				
Db	1	ENPVVHFFKQIVTPRPP	17				

RESULT 4  
 AAE23935  
 ID AAE23935 standard; peptide; 17 AA.

XX AC AAE23935;

DT 10-SEP-2002 (first entry)  
 XX DE Peptide analogue used in the invention.  
 XX KW Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;  
 KW immunoabsorptive; T-cell receptor; therapy.  
 XX OS Unidentified.  
 XX PN WO200216434-A1.  
 XX PD 28-FEB-2002.  
 XX PR 22-AUG-2000; 2000WO-US022988.  
 XX DR 22-AUG-2000; 2000WO-US022988.  
 XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 XX PI Zhang JZ;  
 XX PT WPI; 2002-454317/4B.  
 XX CC A novel peptide used in the treatment of autoimmune disease e.g. multiple  
 PT sclerosis.  
 XX PS Example 2; Fig 2; 64pp; English.  
 XX CC The invention relates to a peptide used in the treatment of autoimmune  
 disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-  
 CC cell receptor sequence found in some MS patients and methods for its  
 detection. T cell receptors comprise alpha and beta chains, with beta  
 CC chains comprising the following regions from N-terminus to C-terminus:  
 CC Vbeta-Dbeta-Jbeta-Theta. T cell receptors naturally vary in the Vbeta-  
 CC Dbeta-Jbeta region. The peptides of the invention are used for treating  
 CC autoimmune disease e.g. multiple sclerosis. The present sequence is a  
 CC peptide analogue used in the exemplification of the invention  
 XX SQ Sequence 17 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	5	17
Matches	17	Pred. No.	6.1e-09
		Mismatches	0
		Indels	0
		Gaps	0

QY 1 ENPVVHFFKNTVTPRTP 17  
 Db 1 ENPVVHFFKNTVTPRTP 17

RESULT 5  
 ABP97941  
 ID ABP97941 standard; peptide; 17 AA.  
 XX AC ABP97941;  
 XX DT 17-JUN-2003 (first entry)  
 XX DE Amino acid sequence of a glycopeptide.  
 XX KW Glycopeptide; serum; immunoabsorption column; antibody;  
 KW multiple sclerosis.  
 XX OS Synthetic.  
 XX FH Key Modified-site Location/Qualifiers  
 FT 1 /note= "Asn(Glc)"  
 FT 2  
 XX PN WO200300733-A2.  
 XX PD 03-JAN-2003.  
 XX PR 19-JUN-2002; 2002WO-EP006767.  
 XX PR 22-JUN-2001; 2001IT-FI000114.  
 XX PA (UYFI-) UNIV FIRENZE.  
 XX PI Papini AM, Chelli M, Rovero P, Lollini F;  
 XX DR MPI; 2003-354383/33.  
 XX PT Novel glycopeptides comprising a specific tetrapeptide, useful as  
 PT diagnostic tools for identifying multiple sclerosis.  
 XX PN WO2003009887-A2.  
 PS Claim 7; Page 12; 14pp; English.

CC	The present invention relates to glycopeptides (ABR56059-ABR56065). The glycopeptides have high specificity in recognizing autoantibodies involved in multiple sclerosis pathology, and thus are effectively used in diagnosis and treatment for multiple sclerosis									
CC										
CC										
CC										
SQ	Sequence 17 AA:									
Query	Match	100.0%	Score	94	DB	6	Length	17		
QY	Best Local Similarity	100.0%	Pred.	No.	6.1e-09		Mismatches	0	Indels	0
Db	Matches	17	Conservative	0					Gaps	0
RESULT	7									
ID	AAO19672									
ID	AAO19672	standard; peptide; 17 AA.								
XX										
AC	AAO19672;									
XX										
DT	28-MAR-2003	(first entry)								
XX										
DE	Human myelin basic protein MBP minimal epitope.									
XX										
KW	Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;									
KW	Fcepsilon receptor; autoimmune disease; constant region; heavy chain;									
KW	antiarthritic; antiallergic; antiinflammatory; dermatological; GEB2;									
KW	antiarthritic; antirheumatic; antidiabetic; neuroprotective;									
KW	myelin basic protein; minimal epitope.									
OS	Homo sapiens.									
XX										
PN	WO200288317-A2.									
XX										
PD	07-NOV-2002.									
XX										
PP	01-MAY-2002; 2002WO-US013527.									
XX										
PR	01-MAY-2001; 2001US-00847208.									
PR	24-OCT-2001; 2001US-00000439.									
XX										
PA	(REGC ) UNIV CALIFORNIA.									
XX										
PI	Saxon A, Zhang K, Zhu D;									
XX										
DR	WPI; 2003-103456/09.									
XX										
PS	Claim 23; Page 116; 116pp; English.									
XX										
CC	The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specifically binding directly or indirectly to a native IgE receptor (FcepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human myelin basic protein minimal epitope which can be used in a fusion protein of									
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XX	Sequence 17 AA;	SQ	the invention
XX	Query Match	100.0%	Score 94; DB 6; Length 17;
XX	Best Local Similarity	100.0%	Pred. No. 6.e-09;
Matches 17;	Conservative	0;	Mismatches 0;
AC	ADE50773;	Indels 0;	Gaps 0;
XX	ADE50773;		
DT	29-JUN-2004 (first entry)		
XX	Wild-type human myelin basic protein peptide analog.		
XX	KW Human; Th2; immune response; myelin basic protein; peptide analog; proteolysis; multiple sclerosis; neuroprotective; gene therapy.		
XX	OS Homo sapiens.		
XX	PN US2002176866-A1.		
XX	PD 28-NOV-2002.		
XX	PP 20-MAR-2002; 2002US-00104973.		
XX	PR 18-NOV-1994; 94US-00342408.		
PR	20-AUG-1998; 98US-00137759.		
PR	19-APR-1999; 99US-00378244.		
XX	(NEUR-) NEUROCRINE BIOSCIENCES INC.		
XX	PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;		
XX	DR WPI; 2003-615722/58.		
PT	Inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, useful for treating multiple sclerosis, comprises administering an amount of a pharmaceutical composition comprising a peptide analog.		
PT	XX Disclosure; SEQ ID NO 3; 52pp; English.		
PS	XX The invention discloses a method for inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, comprising administering a composition comprising a peptide analog in combination with a carrier/adjuvant or diluent. The peptide analog comprises at least two amino acids selected from residues 83 to 99 of human myelin basic protein, where, the L-lysine at position 91, L-arginine at position 97 or L-threonine at position 95, is altered to another amino acid, and one to three L-amino acids selected from valine at position 86 or 87, histidine at position 88, threonine at position 95 or 98, and proline at 99 are altered to an amino acid other than the amino acid present in the native protein at that position or the L-lysine at position 91 is altered to another amino acid and the N- and/or C-terminal amino acid are altered to another amino acid, such that upon administration of the peptide analog <i>in vivo</i> proteolysis is reduced. The peptide analog comprises 7-17 amino acids and one to four additional altered residues. The N-terminal amino acid is residue 83 of human myelin basic protein. At least one of the additional L-amino acids selected from residues 83 to 90 and 92 to 99 is substituted with a charged amino acid. The method is useful for treating multiple sclerosis using Peptide analogs of human myelin basic protein. The sequence presented is the wild-type human myelin basic protein peptide analog.		

; TYPE: PRT  
; ORGANISM: synthetic construct  
; US-09-836-433-30

Query Match      100.0%; Score 94; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17  
Db      3 ENPVVHFFKNIVTPRTP 19

RESULT 13  
US-09-859-012-35  
; Sequence 35, Application US/09859012  
; Publication No. US20040253652A1  
; GENERAL INFORMATION:  
; APPLICANT: RHODE, PETER  
; APPLICANT: WITTMAN, VAUGHAN  
; APPLICANT: WEIDANZ, JON A.  
; APPLICANT: BURKHARDT, MARTIN  
; APPLICANT: CAED, KIMBERLYN F.  
; APPLICANT: TAL, RONY  
; APPLICANT: ACEVEDO, JORGE  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS  
; FILE REFERENCE: 49444 (71758)  
; CURRENT APPLICATION NUMBER: US/09-859, 012  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 60/206, 920  
; PRIOR FILING DATE: 2000-05-25  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 35  
; LENGTH: 20

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide

US-09-859-012-35

Query Match      100.0%; Score 94; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17  
Db      3 ENPVVHFFKNIVTPRTP 19

RESULT 14  
US-09-859-012-49  
; Sequence 49, Application US/09859012  
; Publication No. US20040253652A1  
; GENERAL INFORMATION:  
; APPLICANT: RHODE, PETER  
; APPLICANT: WITTMAN, VAUGHAN  
; APPLICANT: WEIDANZ, JON A.  
; APPLICANT: BURKHARDT, MARTIN  
; APPLICANT: CAED, KIMBERLYN F.  
; APPLICANT: TAL, RONY  
; APPLICANT: ACEVEDO, JORGE  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS  
; FILE REFERENCE: 49444 (71758)  
; CURRENT APPLICATION NUMBER: US/09-859, 012  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 60/206, 920  
; PRIOR FILING DATE: 2000-05-25  
; NUMBER OF SEQ ID NOS: 49

Software: PatentIn Ver. 2.1

Query Match      100.0%; Score 94; DB 13; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 49  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-081-281-33

Query Match      100.0%; Score 94; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17  
Db      3 ENPVVHFFKNIVTPRTP 19

RESULT 15  
US-10-081-281-33  
; Sequence 33, Application US/10081281  
; Publication No. US20020151707A1  
; GENERAL INFORMATION:  
; APPLICANT: Kindbrogel, Wayne  
; Gross, Jane A.  
; Sheppard, Paul  
; TITLE OF INVENTION: Immune Mediators and Related Methods  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent-In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/081.281  
; FILING DATE: 20-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/261.811A  
; FILING DATE: 03-Mar-1999  
; APPLICATION NUMBER: US 08/480, 002  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/482, 133  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/483, 241  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 60/005, 964  
; FILING DATE: 27-OCT-1995  
; APPLICATION NUMBER: US 08/657, 581  
; FILING DATE: 07-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parent, Annette S.  
; REGISTRATION NUMBER: 42,058  
; TELECOMMUNICATION INFORMATION:  
; REFERENCE/DOCKET NUMBER: 014058-005630US  
; INFORMATION FOR SEQ ID NO: 33:  
; SBQUENCE CHARACTERISTICS:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; SBQUENCE DESCRIPTION: SEQ ID NO: 33:  
; US-10-081-281-33

Query Match      100.0%; Score 94; DB 13; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;

Tue Jun 7 11:11:08 2005

us-10-000-439-13.open.rapb

Page 6

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps , 0;  
QY 1 ENPVHFFKNTPRNP 17  
|||||||  
Db 2 ENPVHFFKNTPRNP 18

Search completed: June 7, 2005, 09:25:08  
Job time : 8.45769 secs

GenCore Version 5.1.6  
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OM protein - protein search, using bw model  
 Run on: June 7, 2005, 09:33:36 ; Search time: 40 Seconds  
 Sequence: (without alignments)  
 Scoring table: 31.726 Million cell updates/sec

Title: US-10-000-439-13  
 Perfect score: 94  
 Sequence: 1 ENPVVHFKNIVTPRTP 17  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 177072

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
 6: /cgn2\_6/ptodata/1/iaa/backfilest1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	94	100.0	17	Sequence 3, Appli
2	94	100.0	17	Sequence 3, Appli
3	89	94.7	17	Sequence 19, Appli
4	87	92.6	17	Sequence 20, Appli
5	82	87.2	15	Sequence 37, Appli
6	82	87.2	15	Sequence 16, Appli
7	82	87.2	15	Sequence 16, Appli
8	82	87.2	15	Sequence 11, Appli
9	82	87.2	16	Sequence 21, Appli
10	77	81.9	15	Sequence 23, Appli
11	77	81.9	15	Sequence 22, Appli
12	76	80.9	14	Sequence 3, Appli
13	76	80.9	14	Sequence 3, Appli
14	75	79.8	17	Sequence 3, Appli
15	75	79.8	17	Sequence 6, Appli
16	75	76.6	13	Sequence 4, Appli
17	72	76.6	13	Sequence 19, Appli
18	71	75.5	17	Sequence 7, Appli
19	71	75.5	17	Sequence 11, Appli
20	70	74.5	14	Sequence 2, Appli
21	70	74.5	14	Sequence 3, Appli
22	69	73.4	17	Sequence 3, Appli
23	68	72.3	13	Sequence 8, Appli
24	68	72.3	13	Sequence 38, Appli
25	68	72.3	13	Sequence 22, Appli
26	66	70.2	17	Sequence 24, Appli
27	3	US-0-9-137-759-5	3	Sequence 5, Appli
		US-0-9-378-244-5		
		US-0-9-378-244-8		
		US-0-8-787-547-38		
		PCT-US94-10257A-22		
		FILE REFERENCE: 690068-405C2		
		CURRENT APPLICATION NUMBER: US/09/318, 244		
		CURRENT FILING DATE: 1999-08-19		
		NUMBER OF SEQ ID NOS: 8		
		SOFTWARE: PatentIn Ver. 2.0		
		SEQ ID NO: 3		
		LENGTH: 17		
		TYPE: PRT		
		ORGANISM: Artificial Sequence		
		FEATURE:		
		OTHER INFORMATION: Description of Artificial Sequence: Solid Phase		
		US-09-137-759-3		
		Query Match Score: 94%; DB 3; Length 17;		
		Best Local Similarity: 100.0%; Pred. No. 6.4e-09;		
		Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;		
		Qy: 1 ENPVVHFKNIVTPRTP 17		
		Db: 1 ENPVVHFKNIVTPRTP 17		
		RESULT 2		
		US-09-378-244-3		
		Sequence 3, Application US/09378244		
		Sequence 4, Application US/09378244		
		Patent No. 637970		
		GENERAL INFORMATION:		
		APPLICANT: Gaur, Amitabh		
		APPLICANT: Conlon, Paul J.		
		APPLICANT: Ling, Nicholas C.		
		APPLICANT: Staehlin, Theophil		
		APPLICANT: Crowe, Paul D.		
		TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN		
		CURRENT APPLICATION NUMBER: US/09/318, 244		
		CURRENT FILING DATE: 1999-08-19		

NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 3  
 LENGTH: 17  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
 US-09-378-244-3

Query Match 100.0%; Score 94; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKVNTPRTP 17  
 Db 1 ENPVVHFFKVNTPRTP 17

RESULT 3  
 US-08-468-540B-19  
 ; Sequence 19, Application US/08468540B  
 ; Patent No. 5858980

GENERAL INFORMATION:  
 APPLICANT: Weiner, Howard  
 APPLICANT: Hafler, David  
 APPLICANT: Miller, Ariel  
 APPLICANT: Al-Sabagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 NUMBER OF SEQUENCES: 25  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Darby & Darby P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 COMPUTER: IBM Compatible  
 COMPUTER: Diskette  
 COMPUTER: DOS  
 OPERATING SYSTEM: DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08468,540B  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jacobs, Seth H  
 REGISTRATION NUMBER: 32,140  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-527-7700  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5858980E  
 US-08-468-540B-20

RESULT 4  
 US-08-468-540B-20  
 ; Sequence 20, Application US/08468540B  
 ; Patent No. 5858980

GENERAL INFORMATION:  
 APPLICANT: Weiner, Howard  
 APPLICANT: Hafler, David  
 APPLICANT: Miller, Ariel  
 APPLICANT: Al-Sabagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 NUMBER OF SEQUENCES: 25  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Darby & Darby P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 COMPUTER: IBM Compatible  
 COMPUTER: Diskette  
 COMPUTER: DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08468,540B  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jacobs, Seth H  
 REGISTRATION NUMBER: 32,140  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-527-7700  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5858980E  
 US-08-468-540B-19

RESULT 5  
 US-08-787-547-37  
 ; Sequence 37, Application US/08787547  
 ; Patent No. 5783567

GENERAL INFORMATION:  
 APPLICANT: Hedley, Mary Lynne  
 APPLICANT: Curley, Joanne M.  
 APPLICANT: Langer, Robert S.  
 TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
 TITLE OF INVENTION: OF NUCLEAR ACID  
 NUMBER OF SEQUENCES: 107  
 CORRESPONDENCE ADDRESS:

Query Match 94.7%; Score 89; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NPVWIFFKVNTPRTP 17  
 Db 2 ENPVVHFFKVNTPRTP 17

ADDRESSEE: Fish & Richardson, P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/787,547  
 FILING DATE: 22-JAN-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-542-5070  
 TELEFAX: 617-542-8906  
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-787-547-37

Query Match 87.2%; Score 82; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVWHFFKNTVTPR 15  
 Db 1 ENPVWHFFKNTVTPR 15

RESULT 6  
 US-08-468-540B-16  
 ; Sequence 16, Application US/08468540B  
 ; Patent No. 5858980  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weintraub, Howard  
 ; APPLICANT: Hafler, David  
 ; APPLICANT: Miller, Ariel  
 ; APPLICANT: Al-Sabbagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Darby & Darby P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/400,796

FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: TWOMEY, MICHAEL J.  
 REGISTRATION NUMBER: 38,349  
 REFERENCE/DOCKET NUMBER: R0498/7015  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-720-3500  
 TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 ORGANISM: HOMO SAPIENS

US-08-400-796-16

Query Match 87.2%; Score 82; DB 2; Length 15;



Query Match 81.9%; Score 77; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NPVHFRKNIVTPR 15  
 Db 1 NPYVHFRKNIVTPR 14

RESULT 11  
 US-08-468-540B-22  
 Sequence 22, Application US/08468540B  
 Patent No. 5858980

GENERAL INFORMATION:  
 APPLICANT: Weiner, Howard  
 APPLICANT: Haffler, David  
 APPLICANT: Miller, Ariel  
 APPLICANT: Al-Sabbagh, Ahmad  
 TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
 TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED and BERRY LLP  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Patentnet Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/342,408B  
 FILING DATE: 18-NOV-1994  
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
 NAME: No. 63294997enburg, Carol  
 REGISTRATION NUMBER: 39,317  
 REFERENCE/DOCKET NUMBER: 690068.405  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

US-08-342-408B-3

Query Match 80.9%; Score 76; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WHFFRNIVTPRTP 17  
 Db 1 VHFFRNIVTPRTP 14

RESULT 13  
 US-09-009-953-3  
 Sequence 3, Application US/0900953  
 Patent No. 6413517

GENERAL INFORMATION:  
 APPLICANT: Sette, Alessandro  
 TITLE OF INVENTION: Identification of Broadly  
 Reactive DR Restricted Epitopes  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009,953  
 FILING DATE: 21-Jan-1998  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/036,713

RESULT 12  
 US-08-342-408B-3  
 Sequence 3, Application US/08342408B  
 Patent No. 6329499

GENERAL INFORMATION:  
 APPLICANT: Ling, Nicholas  
 APPLICANT: Gaur, Amitabh

RESULT 11  
 US-08-468-540B-22  
 Sequence 22, Application US/08468540B  
 Patent No. 5858980

GENERAL INFORMATION:  
 APPLICANT: Steinman, Lawrence  
 TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE  
 TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED and BERRY LLP  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentnet Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/342,408B  
 FILING DATE: 18-NOV-1994  
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
 NAME: No. 63294997enburg, Carol  
 REGISTRATION NUMBER: 39,317  
 REFERENCE/DOCKET NUMBER: 690068.405  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

US-08-342-408B-3

Query Match 80.9%; Score 76; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WHFFRNIVTPRTP 17  
 Db 1 VHFFRNIVTPRTP 14

RESULT 13  
 US-09-009-953-3  
 Sequence 3, Application US/0900953  
 Patent No. 6413517

GENERAL INFORMATION:  
 APPLICANT: Sette, Alessandro  
 TITLE OF INVENTION: Identification of Broadly  
 Reactive DR Restricted Epitopes  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009,953  
 FILING DATE: 21-Jan-1998  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997  
 APPLICATION NUMBER: US 60/037,432  
 FILING DATE: 07-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Eileen Lauver  
 REGISTRATION NUMBER: 32,762  
 REFERENCE/DOCKET NUMBER: 018623-011520US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 TELEFAX: 415-576-0300  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-009-953-3

Query Match 80.9%; Score 76; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VVHFFKNIIVTPRTP 17  
 Db 1 VVHFFKNIIVTPRTP 14

RESULT 14  
 US-09-137-759-6  
 Sequence 6, Application US/09137759  
 ; PATENT NO. 6251396  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaur, Amitabh  
 ; APPLICANT: Conlon, Paul J.  
 ; APPLICANT: Ling, Nicholas C.  
 ; APPLICANT: Staehlin, Theophil  
 ; APPLICANT: Crowe, Paul D.  
 ; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING FILE REFERENCE: 690068.405C1  
 ; CURRENT APPLICATION NUMBER: US/09/137,759  
 ; CURRENT FILING DATE: 1998-08-20  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: MOD RES  
 ; LOCATION: (1)  
 ; OTHER INFORMATION: Where Xaa is a D-alanine residue  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
 ; OTHER INFORMATION: Synthesis

US-09-378-244-6  
 Query Match 79.8%; Score 75; DB 3; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 8e-06;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVHFFKNIIVTPRTP 17  
 Db 2 NPVHFFKNIIVTPRTP 17

Search completed: June 7, 2005, 09:39:12  
 Job time : 41 SECs

Query Match 79.8%; Score 75; DB 3; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 8e-06;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 NAME: MOD\_RES  
 LOCATION: (1)  
 OTHER INFORMATION: Where Xaa is a D-alanine residue  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
 OTHER INFORMATION: Synthesis

US-09-137-759-6

RESULT 15  
 US-09-370-244-6  
 ; Sequence 6, Application US/09378244  
 ; Patent No. 6379670

KW	Myelin basic protein; MBP; human; immunodominant region; inhibitor;	PF	05-MAY-1999;	99WO-US009930.
KW	immunosuppressant agent; multiple sclerosis; T cell proliferation;	XX		
KW	suppressor inducer.	PR	05-MAY-1998;	98US-00073109.
OS	Homo sapiens.	XX		
XX	US5858980-A.	PA	(CORI-) CORIXA CORP.	
XX	PN	PI	Arimilli S., Deshpande S;	
XX	PD	DR		
XX	12-JAN-1999.	XX		
XX	06-JUN-1995;	XX		
PP	95US-00468540.	PT	Novel peptides for treating autoimmune diseases of central nervous system characterized by demyelination.	
XX	PR	XX		
XX	30-MAR-1990;	PS	Example 1; Fig 1A; 57pp; English.	
XX	90US-00502559.	XX		
XX	28-FEB-1992;	CC	The invention provides novel peptides derived from human myelin basic protein having an amino acid sequence Phe-X-Lys-Asn-Ile-Val-X-X-X-Thr-X-	
XX	92US-00843752.	CC	X, where X is any amino acid. The MBP peptides are used in the treatment of autoimmune mediated demyelinating disease like multiple sclerosis or	
XX	09-APR-1992;	CC	the murine demyelinating experimental autoimmune encephalomyelitis. The therapeutic compositions comprising novel MBP peptides are used for	
XX	93US-00046354.	CC	inducing oral tolerance or general tolerance. The compositions are used to downregulate or eliminate autoreactive components of the immune system and treat autoreactive demyelinating T-cell mediated immune response.	
XX	09-APR-1993;	CC	The novel MBP peptides when administered into a subject are useful for inhibiting a T-cell mediated immune response against MBP, to treat the T-cell mediated immune response which causes a pathological condition of the nervous system e.g., multiple sclerosis. Prevention or suppression of	
XX	(AUTO-) AUTOIMMUNE INC.	CC	MHC-restricted immune responses is done without any undesirable side effects, such as non-specific suppression of an individual's overall immune response. The MBP peptides provide a safer and more effective treatment by selectively suppressing autoimmune responses at the helper CC	
XX	Miller A., Weiner HL, Hafler DA, Al-Sabbagh A;	CC	CC	
XX	XX	CC	CC	
XX	WPI; 1999-119958/10.	CC	CC	
PT	New peptides from immunodominant regions of human myelin basic protein - useful as immunosuppressants for treatment of multiple sclerosis.	CC	CC	
XX	Claim 1; Col 37; 32pp; English.	CC	CC	
PS		CC	CC	
PS	This sequence represents a fragment of the human myelin basic protein responsive to MBP (or tissues containing it), specifically for treatment of multiple sclerosis (MS). They either induce anergy in MBP-reactive T cells or actively suppress these cells by inhibiting their proliferation, possibly by inducing suppressor T cells. The peptides may also be used to detect specific T cells. The MBP fragments do not induce 'global' immunosuppression upon prolonged use (increasing the risk of a patient developing certain malignancies), will not down regulate normal immune responses to pathogenic micro-organisms and are less toxic than drugs currently used for the treatment of MS, such as azathioprine (Imuran), and cyclosporin A.	CC	CC	
SQ	Sequence 17 AA;	CC	CC	
Query Match	94.7%; Score 89; DB 2; length 17;	CC	CC	
Best Local Similarity	100.0%; Pred. No. 4.4e-08;	CC	CC	
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	CC	
Qy	2 NPVTHFFGNIVTPRTP 17	CC	CC	
Db	1 NPVWHFFKNIVTPRTP 16	CC	CC	
RESULT 14	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AY66534 standard; peptide; 17 AA.	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX		Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		Qy	2 NPVVARFKNTVTPRTP 17	
XX		Db	1 NPVWHFFKNIVTPRTP 16	
RESULT 15	AY66534	Query Match	94.7%; Score 89; DB 3; length 17;	
ID	AAR4118	Best Local Similarity	100.0%; Pred. No. 4.4e-08;	
XX				

XX  
DR  
XX  
PT New peptide (S) derived from human myelin basic protein - used for  
suppressing auto-immune response, partic. in treating multiple sclerosis.  
XX

PS Claim 1; Page 29; 118pp; English.  
XX  
CC The peptide represents residues 84-100 of human myelin basic protein  
(hMBP). The fragment comprises an immunodominant epitope of hMBP which  
CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
CC T-cell line assays. The peptide can be used to stop proliferation of such T-  
CC human T-cells specific for MBP or to elicit active suppression of such T-  
CC cells. They are also used partic. for the treatment of multiple  
CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
CC reactive with MBP. See also AAR4114-25. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX

SQ Sequence 17 AA;

Query Match 92.6%; Score 87; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.7e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHRRPKNIVTPRT 16  
Db 2 ENPVVHFFKNIVTPRT 17

Search completed: June 7, 2005, 09:38:28

Job time : 70 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:38:56 ; Search time 8.63212 Seconds  
 (without alignments)  
 761.681 Million cell updates/sec

Title: US-10-000-439-13  
 Perfect score: 94  
 Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLASTM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq16Dec04:  
 1: geneseqp1980s:  
 2: geneseqp1990s:  
 3: geneseqp2000s:  
 4: geneseqp2001s:  
 5: geneseqp2002s:  
 6: geneseqp2003as:  
 7: geneseqp2003bs:  
 8: geneseqp2004s:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	RESULT 1
1	94	100.0	17	3	AYV69395 Peptide d Myelin ba
2	94	100.0	17	5	AQ020308 Aae26359 Peptide r Peptide a
3	94	100.0	17	5	AAB23935 Ahp97941 Amino aci
4	94	100.0	17	6	ABR56063 Aao19672 Human mye
5	94	100.0	17	6	Ade5073 Wild-type Adk67704 Human mye
6	94	100.0	17	7	ABR50773 DR
7	94	100.0	17	8	ADL18291 Human mye
8	94	100.0	17	8	ARR4115 Human mye
9	94	100.0	17	8	ARR95357 Residues
10	94	100.0	17	8	ARR95357 Human mye
11	94	100.0	18	2	ARR73600 AYX66533 Myelin ba
12	94	100.0	18	2	ARR95357 Sequence
13	94	100.0	18	2	AYX66533 Sequence
14	94	100.0	18	3	AYX66533 Myelin ba
15	94	100.0	19	2	ARR32295 ARR4114 Human mye
16	94	100.0	19	2	ARR4114 Human mye
17	94	100.0	19	2	ARR4123 Human mye
18	94	100.0	19	2	ARR85132 Human MBP
19	94	100.0	19	2	AYW05719 Residues
20	94	100.0	19	2	AYR95366 Residues
21	94	100.0	19	2	AYR95355 Residues
22	94	100.0	19	2	AYR95358 Residues
23	94	100.0	19	2	AYW34183 Br-MBP(84)
24	94	100.0	19	2	AYW34180 Residues
25	94	100.0	19	2	AYW18021 Human BPP
26	94	100.0	19	2	AYW44071 Human mye
27	94	100.0	19	2	AYW73607 Human mye
28	94	100.0	19	2	AYW73616 Human mye
29	94	100.0	19	3	AYY5892 Human MBP
30	94	100.0	19	3	AYY85560 Human MBP
31	94	100.0	19	3	AYY85550 Human MBP
32	94	100.0	19	3	AYY66532 Myelin ba
33	94	100.0	19	3	AYY66543 Myelin ba
34	94	100.0	19	3	AAB12618 Human mye
35	94	100.0	19	3	AAB12613 Vaccine r
36	94	100.0	19	4	AAM9040 Ab71440 ovalbumin
37	94	100.0	19	4	AAG65171 Aag6171 Myelin ba
38	94	100.0	19	4	AAG65171 Abg31655 Myelin ba
39	94	100.0	20	2	AAR94618 Aar9618 Myelin ba
40	94	100.0	20	2	AAR95392 Aar9392 Residues
41	94	100.0	20	2	Raw3187 Br-MBP(83)
42	94	100.0	20	2	Raw3188 Br-MBP(83)
43	94	100.0	20	2	Raw3185 Br-MBP(83)
44	94	100.0	20	2	Raw3184 Br-MBP(83)
45	94	100.0	20	2	Raw3185 Br-MBP(83)

Raw44071 Human mye  
 Raw73607 Human mye  
 Raw73616 Human mye  
 Aay5892 Myelin ba  
 Aay85560 Human MBP  
 Aay85550 Human MBP  
 Aay66532 Myelin ba  
 Aay66543 Myelin ba  
 Aab12618 Human mye  
 Aab12613 Vaccine r  
 Aab12613 Human mye  
 Aam9040 Ovalbumin  
 Aag6171 Myelin ba  
 Abg31655 Myelin ba  
 Aar9618 Myelin ba  
 Aar9392 Residues  
 Aar9392 Residues  
 Raw3187 Br-MBP(83)  
 Raw3188 Br-MBP(83)  
 Raw3185 Br-MBP(83)  
 Raw3184 Br-MBP(83)  
 Raw3185 Br-MBP(83)

The present sequence represents a peptide derived from human myelin basic protein. Myelin basic protein is found in the cytoplasm of human oligodendroglial cells. Peptide analogue derived from the present sequence are administered to a patient in need to induce a Th2 immune response (i.e. production of T cells producing one or more Th2-type cytokines) and/or a persistent systemic immune response to myelin basic protein. These peptide analogues are at least seven amino acids long, derived from residues 83-99 of human myelin basic protein and altered from the native sequence at least at positions 91, 95 or 97. The peptide

CC analogs are especially useful in the treatment of multiple sclerosis  
 XX SQ Sequence 17 AA;

XX Sequence 17 AA;

Query Match 100.0%; Score 94; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKQIVTPRTP 17  
 Db 1 ENPVVHFFKQIVTPRTP 17

RESULT 2  
 AAO20308  
 ID AAO20308 standard; peptide; 17 AA.

AC AAE26359;  
 XX  
 DT 31-MAY-2002 (first entry)  
 DE Myelin basic protein (MBP) apitope peptide region 83-99.  
 KW MBP; myelin basic protein; apitope; antiasthmatic; tolerogenic peptide;  
 KW dermatological; antiallergic; neuroprotective; antithyroid; antianæmic;  
 KW vasotropic; antiinflammatory; immunosuppressive; antidiabetic; class I;  
 KW major histocompatibility complex; MHC; Class II; autoimmune thyroiditis;  
 KW hypersensitivity disorder; antigen; allergy; extrinsic asthma; urticaria;  
 KW autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;  
 KW autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;  
 KW systemic sclerosis; polymyositis; diabetes; transplant rejection;  
 KW antiviral CD8+.  
 XX Unidentified.  
 OS XX  
 PN WO20021610-A2.  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-GB003702.  
 PR XX  
 21-AUG-2000; 2000GB-0020618.  
 PR XX  
 14-JUN-2001; 2001GB-0014547.  
 PA (UVRB-) UNIV BRISTOL.  
 PI Wraith DC, Anderton SM, Mazza G, Ponsonby M, Streeter HB,  
 XX DR  
 XX  
 PT WPI; 2002-292056/33.

XX Selecting tolerogenic peptide useful for treating autoimmune diseases  
 PT e.g., multiple sclerosis, involves selecting peptide which binds major  
 PT histocompatibility complex class I or II molecule without further  
 PT processing.  
 XX  
 PS Claim 12; Page 28; 55pp; English.

XX The invention relates to a method for selecting a tolerogenic peptide,  
 CC comprising selecting a peptide which is capable of binding to a major  
 CC histocompatibility complex (MHC) class I or II molecule without further  
 CC processing. The peptides of the invention are useful for preventing a  
 CC disease such as hypersensitivity disorder, and also for treating and/or  
 CC preventing a disease in a subject. The method involves identifying an  
 CC antigen for the disease, identifying an apitope (antigen processing  
 CC independent epitope) for the antigen, and administering the apitope to  
 CC the subject. The peptides of the invention are also useful for treating  
 CC allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,  
 CC urticaria, autoimmune diseases such as multiple sclerosis, autoimmune  
 CC thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune  
 CC haemolytic anaemia, polymyositis, diabetes, etc., and transplant  
 CC rejection. The peptides are also useful for modifying antiviral CD8+  
 CC responses in a tolerogenic fashion. This sequence represents an apitope  
 CC of the invention of peptide region 83-99 of myelin basic protein (MBP)

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKQIVTPRTP 17  
 Db 1 ENPVVHFFKQIVTPRTP 17

RESULT 3  
 AAE26359;  
 ID AAE26359 standard; peptide; 17 AA.

AC AAE26359;  
 XX  
 DT 13-DEC-2002 (first entry)  
 DE Peptide related to myelin basic protein.  
 KW Th2 immune response; myelin basic protein; MBP; vaccine; MS;  
 KW multiple sclerosis; ant sclerotic.  
 KW OS Unidentified.  
 XX US6379670-B1.  
 PN XX  
 PD 30-APR-2002.  
 PR XX  
 PR 19-AUG-1999; 99US-00378244.  
 PR XX  
 PR 18-NOV-1994; 94US-00342408.  
 PR XX  
 PR 20-AUG-1998; 98US-00137759.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA (NOVS-) NOVARTIS AG.  
 XX  
 PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
 XX DR  
 XX  
 PT Inducing Th2 immune responses to Myelin Basic Protein (MBP) by  
 PT administering the MBP peptide analog CGP 77116, useful for treating  
 PT Multiple Sclerosis.  
 XX  
 RS Disclosure; Col 35-36; 49pp; English.

XX The present invention relates to a novel method for inducing Th2 immune  
 CC responses to Myelin Basic Protein (MBP), or a peptide analogue of MBP in a  
 CC patient. The method involves administering a composition comprising the  
 CC MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for  
 CC treating multiple sclerosis (MS). Sequences of the invention are also  
 CC used as vaccines. The present sequence is a peptide related to human MBP  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKQIVTPRTP 17  
 Db 1 ENPVVHFFKQIVTPRTP 17

RESULT 4  
 AAE23935;  
 ID AAE23935 standard; peptide; 17 AA.

AC AAE23935;

DT	10-SEP-2002	(first entry)
DE	Peptide analogue used in the invention.	
XX		
KW	Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;	
XX	immunosuppressive; T-cell receptor; therapy.	
XX	Unidentified.	
XX		
XX	WQ200216434-A1..	
XX		
XX	PD 28-FEB-2002.	
XX		
PF	22-AUG-2000; 2000WO-US022988.	
XX		
PR	22-AUG-2000; 2000WO-US022988.	
XX		
PA	(BAYU ) BAYLOR COLLEGE MEDICINE.	
XX		
PI	Zhang JZ;	
XX		
PT	WPI; 2002-454317/48.	
XX		
CC	A novel peptide used in the treatment of autoimmune disease e.g. multiple	sclerosis.
CC		
CC	XX	
CC	PS Example 2; Fig 2; 64pp; English.	
CC		
CC	The invention relates to a peptide used in the treatment of autoimmune	disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-
CC	cell receptor sequence found in some MS patients and methods for its	detection. T cell receptors comprise alpha and beta chains, with beta
CC	chains comprising the following regions from N-terminus to C-terminus:	Vbeta-Dbeta-Beta-Cbeta. T cell receptors naturally vary in the Vbeta-
CC	Beta-Beta region. The peptides of the invention are used for treating	autoimmune disease e.g. multiple sclerosis. The present sequence is a
CC	peptide analogue used in the exemplification of the invention	
XX		
SQ	Sequence 17 AA;	
Query Match	100.0%	Score 94; DB 5; Length 17;
Best Local Similarity	100.0%	Pred. No. 6.1e-09; Mismatches
Matches	17; Conservative	0; Indels 0; Gaps 0;
QY	1 ENPVVHFFKNIIVTPRTP 17	
Db	1 ENPVVHFFKNIIVTPRTP 17	
RESULT 5		
ABP97941	ABP97941 standard; peptide; 17 AA.	
ID		
XX		
AC	ABP97941;	
XX		
DT	17-JUN-2003 (first entry)	
DE	Amino acid sequence of a glycopeptide.	
XX		
KW	Glycopeptide; serum; immunoabsorption column; antibody;	
XX	multiple sclerosis.	
OS	Synthetic.	
PH	Location/Qualifiers	
FT	Key	
FT	Modified-site	2
FT	/note= "Asn(Glc)"	
XX		
PN	WO2003000733-A2.	
XX		
PD	03-JAN-2003.	
XX		
PP	19-JUN-2002; 2002WO-BP006767.	
XX		
PR	22-JUN-2001; 2001IT-FI000114.	
XX		
PA	(UYFI-) UNIV FIRENZE.	
XX		
PT	Papini AM, Chelli M, Rovero P, Lolloi F;	
XX		
DR	WPI; 2003-354383/33.	
XX		
PT	Novel glycopeptides comprising a specific tetrapeptide, useful as	
FT	diagnostic tools for identifying multiple sclerosis.	
XX		
XX	Claim 7; Page 12; 14pp; English.	
PN	WO2003009887-A2.	

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The  
 CC glycopeptides have high specificity in recognizing autoantibodies  
 CC involved in multiple sclerosis pathology, and thus are effectively used  
 CC in diagnosis and treatment for multiple sclerosis  
 XX Sequence 17 AA;

Qy	1 ENPVVHFFKNIVTPTP 17	Score 94; DB 6; Length 17;
Db	1 ENPVVHFFKNIVTPTP 17	Best Local Similarity 100.0%; Pred. No. 6.1e-09; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

ID	AA019672	standard; peptide; 17 AA.
AC	AA019672;	
XX		
DT	28-MAR-2003	(first entry)
DE	Human myelin basic protein MBP minimal epitope.	
XX		
KW	Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;	
KW	Fc epsilon receptor; autoimmune disease; constant region; heavy chain;	
KW	antiasthmatic; antiallergic; antiinflammatory; dermatological; GB2;	
KW	anticarthartic; antirheumatic; antidiabetic; neuroprotective;	
KW	myelin basic protein; minimal epitope.	
OS	Homo sapiens.	
XX		
KW	Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;	
KW	Fc epsilon receptor; autoimmune disease; constant region; heavy chain;	
KW	antiasthmatic; antiallergic; antiinflammatory; dermatological; GB2;	
KW	anticarthartic; antirheumatic; antidiabetic; neuroprotective;	
KW	myelin basic protein; minimal epitope.	
OS	Homo sapiens.	
XX		
PR	WO200288317-A2.	
PD	07-NOV-2002.	
PP	01-MAY-2002; 2002WO-US013527.	
XX		
PR	01-MAY-2001; 2001US-00847208.	
XX		
PR	24-OCT-2001; 2001US-00000439.	
XX		
PA	(RESC ) UNIV CALIFORNIA.	
PT	Saxon A, Zhang K, Zhu D;	
XX		
DR	WPI; 2003-103456/09.	
XX		
PT	New fusion molecules comprising polypeptide sequences that bind to IgG	
PT	inhibitory receptor and native IgE receptor, useful for treating IgE-	
PT	mediated hypersensitivity reactions, e.g. asthma or allergies, or	
PT	autoimmune diseases.	
XX		
PS	Claim 23; Page 116; 116pp; English.	
XX		
CC	The present invention relates to a fusion molecule comprising a first	the invention
CC	polypeptide sequence capable of specific binding to a native IgG	
CC	inhibitory receptor consisting of an immune receptor tyrosine-based	Sequence 17 AA;
CC	functional motif (ITIM), expressed on mast cells, basophils or B cells,	
CC	functionally connected to a second polypeptide sequence capable of	
CC	specific binding directly or indirectly to a native IgE receptor	
CC	(FcpsilonIg). Also provided are nucleotide sequences encoding such a	
CC	fusion protein. The fusion molecules and compositions are useful for	
CC	treating an IgE-mediated biological response, preferably an IgE-mediated	
CC	hypersensitivity reaction, such as asthma, allergic rhinitis, atopic	
CC	dermatitis, severe food allergies, chronic urticaria, angioedema or	
CC	anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,	
CC	type-I diabetes mellitus, or multiple sclerosis, and for preventing of,	
CC	or symptoms resulting from, a type I hypersensitivity reaction in a	
CC	subject receiving immunotherapy. The present sequence is the human myelin	
CC	basic protein minimal epitope which can be used in a fusion protein of	

CC	the invention
XX	Sequence 17 AA;

Query Match 100.0%; Score 94; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.1e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

Qy	1 ENPVVHFFKNIVTPTP 17	Score 94; DB 6; Length 17;
Db	1 ENPVVHFFKNIVTPTP 17	Best Local Similarity 100.0%; Pred. No. 6.1e-09; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

ID	ADE5073	standard; peptide; 17 AA.
AC	ADE5073;	
XX		
AC	ADE5073;	
XX		
DT	29-JAN-2004 (first entry)	
XX		
DB	Wild-type human myelin basic protein peptide analog.	
XX		
KM	Human; TN2; immune response; myelin basic protein; peptide analog;	
KW	proteolysis; multiple sclerosis; neuroprotective; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	US2002176866-A1.	
XX		
PR	28-NOV-2002.	
XX		
PR	20-MAR-2002; 2002US-00104973.	
XX		
PR	18-NOV-1994; 94US-00342408.	
PR	20-AUG-1998; 98US-00137759.	
PR	19-AUG-1999; 99US-00378244.	
XX		
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.	
XX		
PI	Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;	
XX		
DR	WPI; 2003-615722/58.	
XX		
PT	Inducing a Th2 immune response to myelin basic protein or its peptide	
PT	analog in a patient, useful for treating multiple sclerosis, comprises	
PT	administering an amount of a pharmaceutical composition comprising a	
PT	peptide analog.	
XX		
PS	Disclosure; SEQ ID NO 3; 52pp; English.	
XX		
CC	The invention discloses a method for inducing a Th2 immune response to	
CC	myelin basic protein or its peptide analog in a patient, comprising	
CC	administering a composition comprising a peptide analog in combination	
CC	with a carrier/adjuvant or diluent. The peptide analog comprises at least	
CC	7 amino acids selected from residues 83 to 99 of human myelin basic	
CC	protein, where: the L-lysine at position 91, L-arginine at position 97 or	
CC	L-threonine at position 95, is altered to another amino acid, and one to	
CC	three L-amino acids selected from valine at position 86 or 87, histidine	
CC	at position 88, threonine at position 95 or 98, and proline at position	
CC	99 are altered to an amino acid other than the amino acid present in the	
CC	native protein at that position or the L-lysine at position 91 is altered	
CC	to another amino acid and the N- and/or C-terminal amino acid are altered	
CC	to another amino acid, such that upon administration of the peptide	
CC	analog in vivo proteolysis is reduced. The peptide analog comprises 7-17	
CC	amino acids and one to four additional altered residues. The N-terminal	
CC	amino acid is residue 83 of human myelin basic protein. At least one of	
CC	the additional L-amino acids selected from residues 83 to 90 and 92 to 99	
CC	is substituted with a charged amino acid. The method is useful for	
CC	treating multiple sclerosis using peptide analogs of human myelin basic	
CC	protein. The sequence presented is the wild-type human myelin basic	
CC	protein peptide analog.	

SQ	Sequence 17 AA;	CC erythematosus, autoimmune thyroiditis, Grave's disease, inflammatory bowel disease, diabetes and rheumatoid arthritis.
Query	Match Best Local Similarity 100.0%; Pred. No. 6.1e-09; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC
Db	1 ENPVHFFKQIVTPRP 17 1 ENPVHFFKQIVTPRP 17	XX
RESULT	9 ADKE7704	SQ Sequence 17 AA;
ID	ADKE7704 standard; peptide; 17 AA.	CC
XX	ADKE7704;	CC
AC		XX
XX	06-MAY-2004 (first entry)	DT
DE	Human myelin basic protein peptide fragment MBP-1 (aa110-126).	XX
KW	Human; myelin basic protein; vaccine; multiple sclerosis; T cell.	XX
XX	Homo sapiens.	OS
OS	XX	XX
XX	WO2004015070-A2.	PN
XX	19-FEB-2004.	PD
XX	06-AUG-2003; 2003WO-US024548.	PF
XX	08-AUG-2002; 2002US-0402521P.	PR
XX	(BAYU ) BAYLOR COLLEGE MEDICINE. (OPEX-) OPEXA PHARM INC.	PA
XX	Zhang JZ;	PI
XX	WPI; 2004-180654/17.	XX
XX	Isolating one or more T cells specific for an antigen of interest comprises incubating a T cell sample with an antigen, useful for diagnosing or treating multiple sclerosis, psoriasis, thyroiditis, diabetes and rheumatoid arthritis.	PT
XX	Isolating one or more T cells specific for self or autoantigens. This comprises incubating a sample of T cells obtained from a patient with the antigen and selecting T cells that express one or more of first markers selected from CD69, CD4, CD25, CD35 and HLA-DR, and one or more second markers selected from interleukin-2, interleukin-5, tumour necrosis factor alpha, interleukin-10 and interleukin-12. The methods are useful for isolating autoreactive T cells which play a role in the pathogenesis of autoimmune diseases. The methods also permit the diagnosis of autoimmune disease as well as monitoring the progression of the disease and for monitoring the efficacy of treatment. The methods allow the preparation of autologous T cell vaccines for the treatment of T cell related autoimmune diseases. Vaccine preparation involves the isolation of antigen-specific T cells optionally followed by culturing steps which allow the expansion of the population of isolated antigen-specific T cells. An example from the invention describes the isolation of myelin-reactive T cells for T cell vaccination. Peripheral blood mononuclear cells were isolated from the blood of multiple sclerosis patients and incubated with peptides comprising known immunodominant regions of 3 myelin proteins. These included the present peptide, which comprises amino acids 110-126 of human myelin basic protein. Cells were then selected for the expression of gene products indicative of activated T cells, and myelin-reactive T cells were propagated in culture. The methods and compositions of the invention are useful for the diagnosis and/or treatment of autoimmune diseases or T cell associated conditions such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus	CC
XX	The present invention is direct to methods of isolating antigen specific T cells, especially T cells specific for self or autoantigens. This comprises incubating a sample of T cells obtained from a patient with the antigen and selecting T cells that express one or more of first markers selected from CD69, CD4, CD25, CD35 and HLA-DR, and one or more second markers selected from interleukin-2, interleukin-5, tumour necrosis factor alpha, interleukin-10 and interleukin-12. The methods are useful for isolating autoreactive T cells which play a role in the pathogenesis of autoimmune diseases. The methods also permit the diagnosis of autoimmune disease as well as monitoring the progression of the disease and for monitoring the efficacy of treatment. The methods allow the preparation of autologous T cell vaccines for the treatment of T cell related autoimmune diseases. Vaccine preparation involves the isolation of antigen-specific T cells optionally followed by culturing steps which allow the expansion of the population of isolated antigen-specific T cells. An example from the invention describes the isolation of myelin-reactive T cells for T cell vaccination. Peripheral blood mononuclear cells were isolated from the blood of multiple sclerosis patients and incubated with peptides comprising known immunodominant regions of 3 myelin proteins. These included the present peptide, which comprises amino acids 110-126 of human myelin basic protein. Cells were then selected for the expression of gene products indicative of activated T cells, and myelin-reactive T cells were propagated in culture. The methods and compositions of the invention are useful for the diagnosis and/or treatment of autoimmune diseases or T cell associated conditions such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus	CC
XX	Example 1; SEQ ID NO 1; 38pp; English.	XX
XX	04-MAR-2004.	PD
XX	US2004043431-A1.	US
XX	04-MAR-2004.	PD
XX	US2004043431-A1.	US
XX	29-AUG-2002; 2002US-00233892.	PR
XX	(VOJD/) VOJDANI A.	PA
XX	WPI; 2004-313756/29.	XX
XX	Diagnosing likelihood and severity of demyelinating disease, by determining antibodies against neuron-specific antigen, comparing level of detected antibodies with normal level for detecting absence/likelihood of demyelinating disease.	PT
XX	Claim 6; SEQ ID NO 2; 27pp; English.	PS
XX	The present invention relates to a method of diagnosing the likelihood and severity of demyelinating diseases. The method involves determining antibodies against neuron-specific antigen in sample, comparing the level of antibodies with the normal level of antibodies, where normal level of antibodies for neuron-specific antigen indicate optimal conditions, lower than or higher than normal level of antibodies for the antigen indicate an absence of or a likelihood of demyelinating diseases, respectively. The neuron-specific antigen is chosen from myelin basic protein (MBP), myelin oligodendrocyte glycoprotein, myelin associated glycoprotein (MAG), proteolipid protein (PLP), small heat shock protein, transaldolase, glial fibrillary protein, transaldolase, glutamate receptor, and phosphodiesterase. The immunoassay is an enzyme linked immunosorbent assay (ELISA) test. The method is useful for diagnosing the likelihood and severity of demyelinating diseases such as multiple sclerosis in a patient. The present sequence represents a peptide from human MBP.	CC
XX	Sequence 17 AA;	SQ

Query Match 100.0%; Score 94; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; MisMatch 0; Del 0; Insert 0; Gap 0;

Qy 1 ENPVVHFFKNTVTPRTP 17  
 Db 1 ENPVVHFFKNTVTPRTP 17

RESULT 11

AAR4116  
 ID AAR4116 standard; peptide, 17 AA.  
 XX  
 AC AAR4116;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-MAY-1994 (first entry)  
 XX  
 DE Human myelin basic protein residues 86-102.  
 XX  
 KW hMBP; suppression; auto immune response; multiple sclerosis;  
 KW immunodominant epitope; T-cell proliferation; CD4; T-cells.  
 XX  
 OS Homo sapiens.  
 XX  
 WO9321222-A1.  
 XX  
 PR 09-APR-1992; 92US-0085318.

PD 28-OCT-1993.

PF 09-APR-1993; 93WO-US003369.

XX  
 PN WO9321222-A1.

XX  
 DR 1996-04-02.

PA (IMMU-) IMMULOGIC PHARM CORP.  
 XX  
 PI Smilek D, Samson M, Gefter M, Hsu D, Shi J, Pallard X, Devaux B;  
 PI Rothbard J, Franzén H;  
 XX  
 DR 1996-04-02.

PT Myelin basic derived peptide(s) and analogs - used in the treatment of  
 PT Multiple Sclerosis, psoriasis, Graves Disease, etc.  
 XX  
 PS Claim 8; Fig 14; 91pp; English.

XX  
 CC AAR95334-R95374 represent peptides derived from myelin basic protein  
 CC (MBP). Immunization with MBP can be used to induce experimental allergic  
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4<sup>+</sup>T<sub>1</sub>  
 CC mediated autoimmune disease which results in demyelination of the  
 CC central nervous system, resulting in paralysis and other neurological  
 CC abnormalities. EAE is a commonly used animal model for human multiple  
 CC sclerosis (MS). These sequences can be used in compositions for treating  
 CC MS in a mammal. The composition acts to down regulate the autoimmune  
 CC response, and may be administered in an amount sufficient to prevent the  
 CC onset of symptoms of MS. The compositions may also be used to treat  
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
 CC MS or benign MS. These Peptides may also be used in the treatment of  
 CC other diseases involving myelin autoantigens, including diabetes, Graves  
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
 CC thymiditis, and rheumatoic arthritis. Peptides derived from other myelin  
 CC autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid  
 CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as  
 CC alternatives to these MBP peptides in these compositions  
 XX  
 SQ Sequence 17 AA:

The peptide represents residues 86-102 of human myelin basic protein  
 (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
 was identified by overlapping 20-mer oligopeptide sequence analysis using  
 T-cell line assays. The Peptide can be used to stop proliferation of such T-  
 cells. They are also used partic. for the treatment of multiple  
 sclerosis. The peptide is also useful for identifying CD4+ T-cells  
 reactive with MBP. See also AAR4114-25. (Updated on 25-MAR-2003 to  
 correct PN field.)

XX  
 SQ Sequence 17 AA:

Query Match 94.7%; Score 89; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; MisMatch 0; Del 0; Insert 0; Gap 0;

Qy 2 NPYVHFFKNTVTPRTP 17  
 Db 1 NPYVHFFKNTVTPRTP 16

RESULT 12

AAR95360  
 ID AAR95360 standard; peptide, 17 AA.  
 XX  
 AC AAR95360;  
 XX  
 DT 16-DEC-1996 (first entry)

Human myelin basic protein fragment.

XX  
 DE Residues 84-100 of myelin basic protein.  
 XX  
 KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
 KW CD4<sup>+</sup>; T-cell; autoimmune disease; demyelination; central nervous system;  
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.  
 XX  
 OS Synthetic.

XX  
 PN WO9612737-A2.

XX  
 PD 02-MAY-1996.

XX  
 PR 25-OCT-1995; 95WO-US013682.

XX  
 PR 15-MAR-1995; 95US-00404228.

XX  
 PA (IMMU-) IMMULOGIC PHARM CORP.  
 XX  
 PI Smilek D, Samson M, Gefter M, Hsu D, Shi J, Pallard X, Devaux B;  
 PI Rothbard J, Franzén H;  
 XX  
 DR 1996-04-02.

PT Myelin basic derived peptide(s) and analogs - used in the treatment of  
 PT Multiple Sclerosis, psoriasis, Graves Disease, etc.  
 XX  
 PS Claim 8; Fig 14; 91pp; English.

XX  
 CC AAR95334-R95374 represent peptides derived from myelin basic protein  
 CC (MBP). Immunization with MBP can be used to induce experimental allergic  
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4<sup>+</sup>T<sub>1</sub>  
 CC mediated autoimmune disease which results in demyelination of the  
 CC central nervous system, resulting in paralysis and other neurological  
 CC abnormalities. EAE is a commonly used animal model for human multiple  
 CC sclerosis (MS). These sequences can be used in compositions for treating  
 CC MS in a mammal. The composition acts to down regulate the autoimmune  
 CC response, and may be administered in an amount sufficient to prevent the  
 CC onset of symptoms of MS. The compositions may also be used to treat  
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
 CC MS or benign MS. These Peptides may also be used in the treatment of  
 CC other diseases involving myelin autoantigens, including diabetes, Graves  
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
 CC thymiditis, and rheumatoic arthritis. Peptides derived from other myelin  
 CC autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid  
 CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as  
 CC alternatives to these MBP peptides in these compositions  
 XX  
 SQ Sequence 17 AA:

Query Match 94.7%; Score 89; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; MisMatch 0; Del 0; Insert 0; Gap 0;

Qy 2 NPYVHFFKNTVTPRTP 17  
 Db 1 NPYVHFFKNTVTPRTP 16

RESULT 13

AAW73601  
 ID AAW73601 standard; peptide, 17 AA.  
 XX  
 AC AAW7360;  
 XX  
 DT 18-MAR-1999 (first entry)

Human myelin basic protein fragment.



- DE Myelin basic protein (MBP) (Myelin A1 protein).  
 GN Name=Mbp; Synonyms=Shi;  
 OS Mus musculus (Mouse);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NCBI\_TaxID=10090;  
 RN [1] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RP STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=93050537; PubMed=179125;  
 RA Campagnoni, A.T., Pribyl, T.M., Campagnoni, C.W., Kampf, K.,  
 RA Amur-Umarjee, S., Landry, C.F., Handley, V.W., Newman, S., Garbay, B.,  
 RA Kitamura, K.;  
 RT "Structure and developmental regulation of Goli-mbp, a 105-kilobase  
 gene that encompasses the myelin basic protein gene and is expressed  
 in cells in the oligodendrocyte lineage in the brain.";  
 RL J. Biol. Chem. 268:4930-4938 (1993).
- [2] SEQUENCE FROM N.A. (ISOFORM 2).  
 RP STRAIN=C57BL/6; TISSUE=Bone marrow;  
 RX MEDLINE=93050537; PubMed=179125;  
 RA Grima, B., Zeilerika, D., Pessac, B.;  
 RT "A novel transcript overcomes the myelin basic protein gene.";  
 RL J. Neurochem. 59:2318-2323 (1992).  
 RN [3] SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 8).  
 RP MEDLINE=86070555; PubMed=2416470; DOI=10.1016/0022-8674(85)90245-4;  
 RA de Ferra, F., Brigh, H., Hudson, L., Kamholz, J., Puckett, C., Molineaux, S.,  
 RA Lazarini, R.A.;  
 RT "Alternative splicing accounts for the four forms of myelin basic  
 protein."; Cell 43:721-727 (1985).  
 RN [4] SEQUENCE FROM N.A. (ISOFORM 5).  
 RP MEDLINE=85254913; PubMed=2410136;  
 RA Takahashi, N., Roach, A., Teplow, D.B., Prusiner, S.B., Hood, L.E.;  
 RT "Cloning and characterization of the myelin basic protein gene from  
 mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate  
 use of exons"; Cell 42:139-148 (1985).  
 RN [5] SEQUENCE FROM N.A. (ISOFORMS 6 AND 7), AND SEQUENCE OF 9-194 FROM N.A.  
 RP STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=87118269; PubMed=2433693;  
 RA Newman, S., Kitamura, K., Campagnoni, A.T.;  
 RT "Identification of a cDNA coding for a fifth form of myelin basic  
 protein in mouse.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890 (1987).  
 RN [6] SEQUENCE FROM N.A. (ISOFORM 8).  
 RP Published=1692584;  
 RA Kimura, K., Campagnoni, A.T.;  
 RA Handley, V.W., Campagnoni, A.T.;  
 RT "Expression of a novel transcript of the myelin basic protein gene.";  
 RL J. Neurochem. 54:2032-2041 (1990).  
 RN [7] SEQUENCE FROM N.A. (ISOFORM 8).  
 RP STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22354883; PubMed=12456851; DOI=10.1038/nature01266;  
 RA Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 RA Nakauchi, I., Ooata, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H.,  
 RA Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T.,  
 RA Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J.,  
 RA Schriml, L.M., Kanapin, A., Matsuda, H., Batyalov, S., Belzel, K.W.,  
 RA Blake, J.A., Brusic, V., Chothia, C., Corrani, L.E., Cousins, S.,  
 RA Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S.,  
 RA Gaertner, T., Garboldi, M., Gibbs, C., Godik, A., Gough, J.,  
 RA Grinnmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D.,  
 RA Kanai, A., Kawaji, H., Kawabawa, Y., Kedzierski, R.M., King, B.L.,  
 RA Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A.,  
 RA Magliocca, D.R., Maltsev, L., Marchionni, L., McKenna, L., Miki, H.,  
 RA Nasashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
 RA Petkovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 RA Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 RA Sandelin, A., Schneider, C., Semple, C.A., Sejnowski, M., Shimada, K.,  
 RA Sultan, R., Takenaka, I., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 RA Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanebe, Y., Weiss, C.,  
 RA Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L.,  
 RA Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N.,  
 RA Hirokane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K.,  
 RA Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S.,  
 RA Hara, A., Hashizume, W., Imotani, K., Isaji, Y., Ichii, M., Kagawa, I.,  
 RA Miyazaki, A., Sakai, K., Sasakai, D., Shitara, K., Shinagawa, A.,  
 RA Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J.,  
 RA Birney, E., Hayashiaki, Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 Nature 420:563-573 (2002)."  
 RL [8] SEQUENCE FROM N.A. (ISOFORM 9).  
 RP TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 RA Klausner, R.D., Collinge, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 RA Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Brat, N.K.,  
 RA Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.J., Heijnen, F.,  
 RA Diachenko, L., Matsusia, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 RA Stapleton, M., Soards, M.B., Ronald, M.F., Casavant, T.L., Schetz, T.B.,  
 RA Brownstein, M.J., Udin, T.B., Toshiyuki, S., Prange, C.,  
 RA Raha, S.S., Louuellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J.,  
 RA Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunnarine, P.H.,  
 RA Richards, S., Worley, P.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 RA Villalon, D.K., Muzyk, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 RA Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A.,  
 RA Whaling, M., Madan, A., Young, C., Shevchenko, Y., Bouffard, G.G.,  
 RA Blakesley, R.W., Torchman, J.W., Green, E.D., Dickson, M.C.,  
 RA Rodriguez, A.C., Grinstein, J., Schmitz, J., Myers, R.M.,  
 RA Butterfield, Y.S.N., Krzywinski, M.I., Yaks, R., Skalska, U., Smalius, D.E.,  
 RA Schnarch, A., Schein, J.E., Jones, S.J.M., Marra, M.A., Smallius, D.E.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [9] SEQUENCE OF 135-157 FROM N.A. (ISOFORMS 4; 6 AND 9).  
 RP MEDLINE=92252919; PubMed=2470651; DOI=10.1016/0378-1119(89)90380-6;  
 RA Milra, M., Tamia, T.A., Royana, A., Mikoshiba, K.;  
 RT "The promoter elements of the mouse myelin basic protein gene function  
 RT efficiently in NG108-15 neuronal/glial cells.";  
 RL Gene 75:31-38 (1991).  
 RN [10] PARTIAL SEQUENCE FROM N.A. (ISOFORMS 4; 6 AND 9).  
 RP MEDLINE=6225971; PubMed=2425537;  
 RA Kamholz, J., de Ferra, F., Puckett, C., Lazzarini, R.A.;  
 RT "Identification of three forms of human myelin basic protein by cDNA  
 cloning.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966 (1986).  
 RN [11] SEQUENCE OF 153-222 FROM N.A. (ISOFORMS 4; 6 AND 9).  
 RP MEDLINE=3411931; PubMed=6138644;  
 RA Zeller, N.K., Hunkele, M.J., Campagnoni, A.T., Sprague, J.,  
 RA Lazzarini, R.A.;  
 RT "Characterization of mouse myelin basic protein messenger RNAs with a  
 RT myelin basic protein cDNA clone.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22 (1984).  
 RN [12] PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).  
 RP TISSUE=Spinal cord;  
 RX MEDLINE=91162193; PubMed=1705957;  
 RA Aruga, J., Okano, H., Mikoshiba, K.;  
 RA "Aruga, J., Okano, H., Mikoshiba, K.;  
 RT "Identification of the new isoforms of mouse myelin basic protein: the  
 RT existence of exon 5a.";  
 RL J. Neurochem. 56:1222-1226 (1991).  
 RN [13] PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12 AND 13).  
 RP TISSUE=Embryonic brain;  
 RX MEDLINE=33203993; PubMed=7681106;

- RA Nakajima K., Ikenaka K., Kagawa T., Aruga J., Nakao J., Nakahira K., [1]  
 RA Shioota C., Kim S.U., Mikoshiba K.; "Novel isoforms of mouse myelin basic protein predominantly expressed  
 RT in embryonic stage"; J. Neurochem. 60:1554-1563 (1993).  
 RL [14]
- RP SEQUENCE OF 191-224 FROM N.A.  
 RX MEDLINE=88196094; PubMed=2452084;  
 RA Okano H., Tamura T., Miura M., Aoyama A., Ikenaka K., Oshimura M.,  
 RA Mikoshiba K.; "Gene organization and transcription of duplicated MBP genes of myelin  
 RT deficient (shi(m)) mutant mouse.;" RT  
 RL EMBIO J. 7:77-83 (1988).  
 RN [15]
- RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=98409779; PubMed=9736652;  
 RA Landry C.F., Pribyl T.M., Ellison J.A., Givogri M.I., Kampf K.,  
 RA Campagnoni C.W., Campagnoni A.T.; "Embryonic expression of the myelin basic protein gene: identification  
 RT of a promoter region that targets transgene expression to pioneer  
 RT neurons.;" J. Neurosci. 18:7315-7327 (1998).  
 RL [16]
- RP FUNCTION.  
 RX MEDLINE=21018309; PubMed=1145205;  
 RA Campagnoni A.T., Stooff R.P.; "The pathobiology of myelin mutants reveal novel biological functions  
 RT of the MBP and PLP genes.;" RT  
 RL Brain Pathol. 11:74-91 (2001).
- !- FUNCTION: The classic group of MBP isoforms (isoforms 4-13) are  
 with PLP the most abundant protein components of the myelin  
 membrane in the CNS. They have a role in both its formation and  
 stabilization. The non-classic group of MBP isoforms (isoforms 1-  
 3/Golli-MBPs) may preferentially have a role in the early  
 developing brain long before myelination, "maybe as components of  
 transcriptional complexes, and may also be involved in signaling  
 pathways in T-cells and neural cells. Differential splicing events  
 combined to optional posttranslational modifications give a wide  
 spectrum of isomers, each of them having maybe a specialized  
 function.
- !- SUBUNIT: Homodimer (By similarity)  
 CC isoforms, cytoplasmic and nuclear for non-classic isoforms.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative  
 CC Comment=Additional isoforms seem to exist;  
 Name-1; Synonyms=Golli-MBP1, J37;  
 IsoID=PP4370-1; Sequence=Displayed;
- CC Name-2; Synonyms=Golli-MBP2, BG21, HMBPR;  
 CC Query Match 100.0%; Score 94; DB 1; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2e-07; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENPVVHFFKQIVTPRTP 17  
 Db 214 ENPVVHFFKQIVTPRTP 230
- RESULT 14
- MBP\_HUMAN STANDARD; PRT; 304 AA.  
 ID P02686; Q15337; Q15338; Q15340;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
- DE Myelin basic protein (MBP) (Myelin A1 protein) (Myelin membrane  
 DE encephalitogenic protein).  
 DE Name=MBP;  
 OS Homo sapiens (Human).  
 OC Bokayuta; Metzko; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=9606;
- RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=94068468; PubMed=750278;  
 RA Pribyl T.M., Campagnoni C.W., Kampf K., Kashima T., Handley V.W.,  
 RA McManon J., Campagnoni A.T.; "The human myelin basic protein gene is included within a 179-kilobase  
 RT transcription unit: expression in the immune and central nervous  
 RT systems.;" RT  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699 (1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 3, 4, 5 AND 6).  
 RC TISSUE=Embryonic spinal cord;  
 RX MEDLINE=87311781; PubMed=2442403;  
 RA Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F.,  
 RA Campagnoni A.T.; "Evidence for the expression of four myelin basic protein variants in  
 the developing human spinal cord through cDNA cloning.;" RT  
 RL J. Neurosci. Res. 17:321-328 (1987).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 6).  
 RC TISSUE=Embryonic spinal cord;  
 RX MEDLINE=8638101; PubMed=2427378;  
 RA Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F.,  
 RA Campagnoni A.T.; "Isolation and characterization of a cDNA coding for a novel human  
 RT 17.3K myelin basic protein (MBP) variant.;" RT  
 RL J. Neurosci. Res. 16:227-238 (1986).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 5).  
 RX MEDLINE=86259714; PubMed=24253357;  
 RA Kamholz J., de Perra F., Puckett C., Lazzarini R.A.; "Identification of three forms of human myelin basic protein by cDNA  
 RT cloning.;" RT  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966 (1986).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 3, 4, 5 AND 6).  
 RX MEDLINE=89302693; PubMed=2472816;  
 RA Streicher R., Stoefel W.; "The organization of the human myelin basic protein gene. Comparison  
 RT with the mouse gene.;" RT  
 RL Biol. Chem. Hoppe-Seyler 370:503-510 (1989).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 5).  
 RC TISSUE=Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Reingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schulter G.D.,  
 RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Marszina K., Farmer A.A., Rubin G.M., Hong I.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullabay S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gray L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fabey J., Helton E., Keitteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A. C., Shevchenko A., Bouffard G.G.,  
 RA Blakesley R.W., Tochman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzjwinski M.I., Salska U., Smailus D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.;" RT  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [7]  
 RP SEQUENCE (ISOFORM 5).  
 RX MEDLINE=206600; PubMed=4108501;  
 RA Carnegie P.R.;  
 RT "Amino acid sequence of the encephalitogenic basic protein from human  
 myelin.;" RT  
 Biochem. J. 123:57-67 (1971).

- RN [8]  
 RP SEQUENCE OF 135-192 FROM N.A.  
 RX MEDLINE=90152879; PubMed=1682270;  
 RA Boylan K.B.; Ayres T.M.; Popko B.; Takahashi N.; Hood L.E.,  
 RA Prusiner S.B.;  
 RT "Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a  
 new form of oligonucleotide repetitive sequence showing length  
 polymorphism";  
 RT Genomics 6:16-22 (1990).  
 RN [9]  
 RP SEQUENCE OF 179-222 (ISOFORM 5), AND REVISIONS.  
 RA Shpirka R.; McKneally S.S.; Chou F.; Kibler R.F.;  
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid  
 sequence of bovine rabbit, guinea pig, monkey, and human fragments.;"  
 RL J. Biol. Chem. 246:4630-4640 (1971).  
 RN [10]  
 RP SEQUENCE OF 135-178 AND 224-304 (ISOFORM 3), AND MASS SPECTROMTRY.  
 MEDLINE=86280476; PubMed=2428402;  
 RA Scoble H.A.; Whitaker J.N.; Biemann K.;  
 RT "Analysis of the primary sequence of human myelin basic protein  
 peptides 1-44 and 90-170 by fast atom bombardment mass spectrometry.;"  
 RL J. Neurochem. 47:614-616 (1986).  
 RN [11]  
 RP SEQUENCE OF 148-304 (ISOFORM 5), AND CITRULLINATION OF C8.  
 RC TISSUE=Brain;  
 RX MEDLINE=8917479; PubMed=2466844;  
 RA Wood D.B.; Moscarello M.A.;  
 RT "The isolation, characterization, and lipid-aggregating properties of  
 a citrulline containing myelin basic protein.;"  
 RL J. Biol. Chem. 264:5121-5127 (1989).  
 RN [12]  
 RP SEQUENCE OF 179-223 (ISOFORM 5), AND MASS SPECTROMTRY.  
 RX MEDLINE=8418508; PubMed=620481;  
 RA Gibson B.W.; Gilliom R.D.; Whitaker J.N.; Biemann K.;  
 RT "Amino acid sequence of human myelin basic protein peptide 45-89 as  
 determined by mass spectrometry."  
 RL J. Biol. Chem. 259:5028-5031 (1984).  
 RN [13]  
 RP SEQUENCE OF 246-269 (ISOFORM 3), AND ENCEPHALITOGENIC PEPTIDE.  
 RX MEDLINE=7108805; PubMed=4093924;  
 RA Lenox V.A.; Wilks A.V.; Carnegie P.R.;  
 RT "Immunologic properties of the main encephalitogenic peptide from the  
 basic protein of human myelin.;"  
 RL J. Immunol. 105:1223-1230 (1970).  
 RN [14]  
 RP SEQUENCE OF 156-172 AND 302-304, AND CHARACTERIZATION OF C8.  
 RC TISSUE=Brain;  
 RX MEDLINE=96004793; PubMed=7574672; DOI=10.1006/abbi.1995.1449;  
 RA Boulilas C.; Bang H.; Mastronardi F.; Moscarello M.A.;  
 RT "The isolation and characterization of four myelin basic proteins from  
 the unbound fraction during CMS2 chromatography.;"  
 RL Arch. Biochem. Biophys. 322:174-182 (1995).  
 RN [15]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RX PubMed=6857651;  
 RA Proost P.; Van Damme J.; Opendenaker G.;  
 RT "Leukocyte gelatinase B cleavage releases encephalitogens from human  
 myelin basic protein.;"  
 RL Biochem. Biophys. Res. Commun. 192:1175-1181 (1993).  
 RN [16]  
 RP METHYLATION.  
 RX MEDLINE=72066401; PubMed=5128665;  
 RA Baldwin G.S.; Carnegie P.R.;  
 RT "Isolation and partial characterization of methylated arginines from  
 the encephalitogenic basic protein of myelin.;"  
 RL Biochem. J. 123:69-74 (1971).  
 RN [17]  
 RP STRUCTURE OF 135-149 BY NMR.  
 RX MEDLINE=9537286; PubMed=7544282;  
 RA Mendz G.L.; Barden J.A.; Martenson R.E.;  
 RT "Conformation of tetradecapeptide epitope of myelin basic protein.;"  
 RL Bur. J. Biochem. 231:659-666 (1995).  
 RN [18]  
 RP 3D-STRUCTURE MODELING OF 135-279 (ISOFORM 5).  
 RX MEDLINE=9717499; PubMed=9020143; DOI=10.1074/jbc.272.7.4269;  
 RA Ridderdael R.A.; Beniac D.R.; Tompkins T.A.; Moscarello M.A.; Harauz G.;  
 RT "Three-dimensional structure of myelin basic protein. II. Molecular  
 modeling and considerations of predicted structures in multiple  
 sclerosis.;"  
 RL J. Biol. Chem. 272:4269-4275 (1997).  
 CC -!- FUNCTION: The classic group of MBP isoforms (isoforms 4-14) are  
 with PLP the most abundant protein components of the myelin  
 membrane in the CNS. They have a role in both its formation and  
 stabilization. The smaller isoforms might have an important role  
 in remyelination of denuded axons in multiple sclerosis. The non-  
 classic group of MBP isoforms (isoforms 1-3/Goll-MBP) may  
 preferentially have a role in the early developing brain long  
 before myelination, maybe as components of transcriptional  
 complexes and may also be involved in signaling pathways in T-  
 cells and neural cells. Differential splicing events combined to  
 optional posttranslational modifications give a wide spectrum of  
 isomers, each of them having maybe a specialized function.  
 -!- SUBUNIT: Homodimer (By Similarity).  
 -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
 -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=6;  
 Comment=Additional isoforms seem to exist;  
 Name=1; Synonyms=MBP1; Sequence=vsp\_003308; VSP\_003308;  
 IsoId=P02686-1; Sequence=vsp\_003308; VSP\_003309; VSP\_003310;  
 Name=2; Synonyms=Goll-MBP; Sequence=vsp\_003311;  
 IsoId=P02686-2; Sequence=vsp\_003311;  
 Name=3; Synonyms=MBP1; Sequence=vsp\_003311;  
 IsoId=P02686-3; Sequence=vsp\_003308; VSP\_003309;  
 Name=4; Synonyms=MBP2; Sequence=vsp\_003308; VSP\_003310;  
 IsoId=P02686-4; Sequence=vsp\_003308; VSP\_003310;  
 Name=5; Synonyms=MBP3; Sequence=vsp\_003308; VSP\_003310;  
 Name=6; Synonyms=MBP4; Sequence=vsp\_003308; VSP\_003310;  
 IsoId=P02686-6; Sequence=vsp\_003308; VSP\_003310;  
 RN -!- TISSUE=SPECIFICITY: MBP isoforms are found in both the central and  
 the peripheral nervous system, whereas Goll-MBP isoforms are  
 expressed in fetal thymus, spleen and spinal cord, as well as in  
 cell lines derived from the immune system.  
 -!- DEVELOPMENTAL STAGE: Expression turns on abruptly in fetus of 14  
 Query Match 100.0%; Score 94; DB 1; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy Db 1 ENPVVHFFKQIVTPPTP 17  
 Db 217 ENPVVHFFKQIVTPPTP 233

Search completed: June 7, 2005, 09:01:30  
Job time : 10.3679 secs

RL Glia 2:241-249 (1989).  
 CC -!- FUNCTION: Is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.  
 CC Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Comment=Additional isoforms seem to exist;  
 Name=1;  
 IsoId=P15720-1; Sequence=Displayed;  
 Note=Major isoform;  
 Name=2;  
 IsoId=P15720-2; Sequence=Displayed;

-!- DEVELOPMENTAL STAGE: In the optic lobe, first detected at embryonic day 14. Expression strongly increases between embryonic days 16 and 18, reaches a maximum at postnatal day 1, and then declines again to the adult level.

-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of Serine or Threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.

-!- SIMILARITY: Belongs to the myelin basic protein family.

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CC EMBL: X17103; CAA39959.1; --.  
 DR S08535; S08535.  
 DR HSSP; P03686; IQCL.  
 DR InterPro; IPR00548; Myelin BP.  
 DR Pfam; PF01669; Myelin MBP; I.  
 DR PRINTS; PR00242; MBLINMBP.  
 DR PRODOM; PD004542; Myelin BP; 1.  
 DR PS00569; MYELIN-MBP; 1.  
 DR Acetylation; Alternative splicing; Citrullination; Methylation; Myelin; Phosphorylation; Structural protein.  
 FT INIT\_MET 0 By similarity.  
 FT MOD\_ RES 1 1 N-acetylalanine (By similarity).  
 FT MOD\_ RES 7 7 Phosphoserine (By similarity).  
 FT MOD\_ RES 24 24 Citrulline (By similarity).  
 FT MOD\_ RES 29 29 Diamidated glutamine (partial) (By similarity).  
 FT MOD\_ RES 96 96 Phosphothreonine (By similarity).  
 FT MOD\_ RES 101 101 Diamidated glutamine (partial) (By symmetry).  
 FT MOD\_ RES 105 105 Symmetric dimethylarginine (By similarity).  
 FT MOD\_ RES 113 113 Phosphoserine (By similarity).  
 FT MOD\_ RES 146 146 Diamidated glutamine (partial) (By symmetry).  
 FT MOD\_ RES 164 164 Phosphoserine (By similarity).  
 FT MOD\_ RES 168 168 Phosphoserine (By similarity).  
 FT MOD\_ RES 173 173 Citrulline (By similarity).  
 FT VAR\_SPLIC 104 114 Missing (in isoform 2).  
 SQ SEQUENCE 173 AA; 18677 MW; ABFET70D4C9CF019D CRC64;  
 Query Match 92.6%; Score 87; DB 1; Length 173;  
 Best Local Similarity 88.2%; Pred No. 2.1e-06; Db Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ENPVWHPFKNIVTPRTP 17  
 81 DNPPVHFFKNIVSPRTP 97

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Page 1

RESULT 2  
US-10-000-439-13  
Sequence 13, Application US/10000439  
Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067\_04A  
; CURRENT APPLICATION NUMBER: US/10-000, 439  
; CURRENT FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: US 09/847, 208  
; PRIORITY FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-000-439-13

Query	Match	Score	DB	Length	Matches	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 ENPVVHFFKNIKVTPRTP 17	100.0%	94	14	17	100.0%	4.6e-08	0	0	0	0
Db	1 ENPVVHFFKNIKVTPRTP 17										

RESULT 3  
US-10-362-264-1  
Sequence 1, Application US/10362264  
Publication No. US20030191063A1  
; GENERAL INFORMATION:  
; APPLICANT: Wraith, David  
; APPLICANT: Anderson, Stephen  
; APPLICANT: Mazzia, Graziella  
; APPLICANT: Ponfroid, Mary  
; APPLICANT: Streeter, Heather  
; APPLICANT: The University of Bristol  
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD  
; FILE REFERENCE: 1433\_004US1  
; CURRENT APPLICATION NUMBER: US/10/362, 264  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03702  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 0020618.5  
; PRIOR FILING DATE: 2000-06-21  
; PRIOR APPLICATION NUMBER: 0114547.3  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-362-264-1

Query	Match	Score	DB	Length	Matches	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 ENPVVHFFKNIKVTPRTP 17	100.0%	94	14	17	100.0%	4.6e-08	0	0	0	0
Db	1 ENPVVHFFKNIKVTPRTP 17										

RESULT 4  
US-10-233-892A-2  
Sequence 2, Application US/10233892A  
Publication No. US200404331A1  
; GENERAL INFORMATION:

RESULT 5  
US-10-482-044-5  
Sequence 5, Application US/10482044  
Publication No. US20040235713A1  
; GENERAL INFORMATION:  
; APPLICANT: Anna Maria PAPINI et al  
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or therapeutic treatment of multiple sclerosis  
; FILE REFERENCE: 2784 PTWO  
; CURRENT APPLICATION NUMBER: US/10/482, 044  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: PCT/EP 02/06767  
; PRIOR FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: FI2001A000114  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Glycopeptide  
; FEATURE:  
; NAME/KEY: CARBOHYD  
; LOCATION: (2) .. (2)  
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl  
; US-10-482-044-5

Query	Match	Score	DB	Length	Matches	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 ENPVVHFFKNIKVTPRTP 17	100.0%	94	14	17	100.0%	4.6e-08	0	0	0	0
Db	1 ENPVVHFFKNIKVTPRTP 17										

RESULT 6  
US-09-813-463A-13  
Sequence 13, Application US/09813463A  
Patent No. US20030147303A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; APPLICANT: CATZ, INGRID  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS



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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-872-836-37

Query Match 87.2%; Score 82; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTPR 15
Db 1 ENPVVHFFKNIIVTPR 15

RESULT 11
US-09-739-466C-5
; Sequence 5, Application US/09739466C
; Publication No. US20050107585A1
; GENERAL INFORMATION:
; APPLICANT: MURRAY, JOSEPH S
; APPLICANT: STIRANAN, TERRINA J
; APPLICANT: HU, YONGBO
; CURRENT APPLICATION NUMBER: US/09/739,466C
; TITLE OF INVENTION: SIGNAL-1/SIGNAL-2 BIFUNCTIONAL PEPTIDE INHIBITORS
; FILE REFERENCE: 23902-08805
; CURRENT FILING DATE: 2000-12-18
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-739-466C-5

RESULT 12
US-10-112-654-11
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Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTPR 15
Db 1 ENPVVHFFKNIIVTPR 15

RESULT 13
US-10-056-583-1
Sequence 1, Application US/10056583
Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridakis-Harell, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 1
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Immunodominant peptide of MBP, recognized by
; OTHER INFORMATION: HLA-DR2 haplotype
; NAME/KEY: DOMAIN
; LOCATION: 85 - 99
; US-10-056-583-1

RESULT 14
US-10-239-313A-142
Query Match 87.2%; Score 82; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTPR 15
Db 1 ENPVVHFFKNIIVTPR 15

RESULT 14
US-10-239-313A-142
Query Match 87.2%; Score 82; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTPR 15
Db 1 ENPVVHFFKNIIVTPR 15

RESULT 14
US-10-239-313A-142
Query Match 87.2%; Score 82; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTPR 15
Db 1 ENPVVHFFKNIIVTPR 15

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Db      ||||||| 1 ENPVWHFFKNIVTPR 15
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RESULT 15  
 US-10-362-264-5  
 ; Sequence 5, Application US10362264  
 ; Publication No. US20050191063A1

; GENERAL INFORMATION:

; APPLICANT: Wraith, David  
 ; APPLICANT: Anderson, Stephen  
 ; APPLICANT: Mazza, GrazIELIA

; APPLICANT: Ponsford, Mary  
 ; APPLICANT: Streeter, Heather  
 ; APPLICANT: The University of Bristol

; TITLE OF INVENTION: PEPTIDE SELECTION METHOD  
 ; FILE REFERENCE: 1433.004US1  
 ; CURRENT APPLICATION NUMBER: US10/362,264

; CURRENT FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/03702

; PRIOR FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: 0020618..5

; PRIOR FILING DATE: 2000-08-21  
 ; PRIOR APPLICATION NUMBER: 0114547..3

; PRIOR FILING DATE: 2001-06-14  
 ; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5

; LENGTH: 15  
 ; TYPE: PRT

; ORGANISM: Homo sapiens  
 ; US-10-362-264-5

Query Match 87.2%; Score 82; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0;

Gaps 0; Ov

QY	1 ENPVWHFFKNIVTPR 15
Db	1 ENPVWHFFKNIVTPR 15

Search completed: June 7, 2005, 09:50:47  
 Job time : 144 secs

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0 - 99999 - JWP - 24 - X